

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	840.5	67.5	234	4	Q43404		O43404 homo sapien
2	90	7.2	280	6	Q9MYL6		Q9MYL6 macaca neme
3	89.5	7.2	225	13	Q9IB42		Q9IB42 paralichthy
4	89.5	7.2	401	2	P72902		P72902 synechocyst
5	89.5	7.2	847	14	Q9WTS1		Q9WTS1 human immun
6	89	7.1	169	11	Q9WY90		Q9WY90 marmota mon
7	88	7.1	234	6	Q28320		Q28320 capra hircu
8	87.5	7.0	895	10	Q9M980		Q9M980 arabidopsis
9	87	7.0	2013	5	Q96216		Q96216 plasmodium
10	86.5	6.9	217	11	Q9ER66		Q9ER66 peromyscus
11	86.5	6.9	2195	3	Q02832		Q02832 saccharomyc
12	86	6.9	674	3	Q06629		Q06629 saccharomyc
13	85.5	6.9	873	10	Q9FTD8		Q9FTD8 arabidopsis
14	85	6.8	283	10	Q9FKU2		Q9FKU2 arabidopsis
15	85	6.8	699	14	Q9DP26		Q9DP26 human immun
16	84.5	6.8	208	2	Q88241		Q88241 pantoea cit
17	84.5	6.8	884	10	Q81069		Q81069 arabidopsis
18	84	6.7	282	14	Q9IC83		Q9IC83 kaposi's sa
19	84	6.7	544	14	Q64940		Q64940 avian infec

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Db 55 ATIMVLVORTSIPSPDNVPLKGGNCSDELICLRAPFKKSWAYLQVAKHLNKTLS 114
QY 120 WNEDETHGLIYQDGNLIYQFPGLYFIVCOLQFLVOCNSHSDVLTQLLINSKIKKQTLV 179
Db 115 WNKDGLHGVRYQDGNLIYQFPGLYFIVCOLQFLVOCNPNVDLKKELLINKHKKQXLV 174
QY 180 TVCESGVQSKNIYQNLISQFLLHYLQWNTISVRVDFNQYVDNTFPDNLVSLVFLYSSD 239
Db 175 TVCESGMQTKHYVQNLISQFLLDYLQWNTISVNVDTXQYIDTSTFPLENVLSIFLXNSD 234

RESULT 2
Q9MYL6 PRELIMINARY; PRT; 280 AA.
AC Q9MYL6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE FAS LIGAND.
GN PT-FASL OR CM-FASL OR RM-FASL.
OS Macaca nemestrina (Pig-tailed macaque),
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9545, 9541, 9544;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=M.nemestrina; STRAIN=PTIG-TAILED MONKEY;
RA Kirii Y., Inoue T., Yoshino K.;
RT "Pig-tailed monkey Fas ligand mRNA, complete cds.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=M.fascicularis; STRAIN=CYNOMOLGUS MONKEY;
RA Kirii Y., Inoue T., Yoshino K.;
RT "Cynomolgus monkey Fas ligand mRNA, complete cds.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=M.mulatta; STRAIN=RHEBUS MONKEY;
RA Kirii Y., Inoue T., Yoshino K.;
RT "Rhesus monkey Fas ligand mRNA, complete cds.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB035140; BAA90296.1; -
DR EMBL; AB035138; BAA90294.1; -
DR EMBL; AB035139; BAA90295.1; -
DR InterPro; IPR000478; -
DR Pfam; PF00229; TNF_1;
DR PRINTS; PR01234; TNECROSISFCT.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
SQ SEQUENCE 280 AA; 31367 MW; F0B284D61A132EB4 CRC64;

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Query Match 7.2%; Score 90; DB 6; Length 280;
Best Local Similarity 21.1%; Pred. No. 0.84;
Matches 52; Conservative 37; Mismatches 75; Indels 82; Gaps 12;

QY 14 PSPDPAMQVQGVASVPMRSTRPWRSTRSYFYLTALVCLVAVAILVLV----- 67
Db 59 PSLPPLPLPP-----LKKRGHSTG-----LCLLVFFWLVVALVGLGLGM 100

QY 68 -----QKSDTPNTEKAPLKGNCSEDLFCFLKS-----TPSKSW---AYLQVSK 111
Db 101 FOLFHLQK-----ELAELESTSQKHTASSLEKQIGHPSPPEKKEQKVAHLTGK 152

QY 112 HLNNTKLKSWNEDGTI---HGLIYQDGNLIYQFPGLYFIVCOLQFLVQ-CSN-----HSDVL 163
Db 153 NSRSMPLWEDTYGIVLISGVKRYKKGGLVNETGLYFVYKSVYFRQSGCTNPLSHKV-- 210

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QY 164 TLQLLINSK-----IKKOTLVTVCESG-----VQSKNIYQNLISQFLLHY 202
Db 211 ---YMRNYSKPDQLYMMEKGMNYSCTTGOMWASHSYLGAVFNLTSADHLYVNVSELSYN 267
QY 203 LQVNST 208
Db 268 FEESOT 273

RESULT 3
Q9IB42 PRELIMINARY; PRT; 225 AA.
AC Q9IB42;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE TUMOR NECROSIS FACTOR.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Bothidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RA Hirono I., Nam B., Kurobe T., Aoki T.;
RT "Molecular cloning, characterization and expression of tumor necrosis
factor (TNF) cDNA and gene from Japanese flounder Paralicthys
olivaceus.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040448; BAA94969.1; -
DR InterPro; IPR000478; -
DR Pfam; PF00229; TNF_1;
DR PRINTS; PR01234; TNECROSISFCT.
DR PROSITE; PS00049; TNF_2; 1.
SQ SEQUENCE 225 AA; 24965 MW; 8F947FB25FC82658 CRC64;

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Query Match 7.2%; Score 89.5; DB 13; Length 225;
Best Local Similarity 25.4%; Pred. No. 0.74;
Matches 31; Conservative 23; Mismatches 57; Indels 11; Gaps 5;

QY 52 LVCLVAVAILVLVQKKDSTPNTTEKAPLKGNCSE--DLFCTLKTPSK-KSWAYL- 107
Db 10 IVALCLGVLAFAFWYTNKSEMNTGQTAALSKQCAEKTEPHNTLRQISSRAKAAIHLE 69

QY 108 ---QVSKHLNNTKLSW-NEDG---TIHGLIYQDGNLIYQFPGLYFIVCOLQFLVOCNSH 160
Db 70 GRDEDEETSENKLVWKNDEGLAFTQGGFELVDNHHIIPRSLGLYFVYQSAPRVSDD 129

QY 161 VD 162
Db 130 AD 131

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RESULT 4
P72902 PRELIMINARY; PRT; 401 AA.
AC P72902;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE HYPOTHETICAL 46.0 KDA PROTEIN.
GN SLR1066.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hiroseawa M., Sugliura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakasaki N., Naruo K., Okumura S.,

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RA Shimp S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL: D90901; BAA16918.1; -
DR InterPro: IPR001296; -
DR Pfam: PF00534; Glycos_transf_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 401 AA; 45951 MW; 9A8C3E0C64933271 CRC64;

Query Match 7.2%; Score 89.5; DB 2; Length 401;
Best Local Similarity 26.6%; Pred. No. 1.4;
Matches 42; Conservative 13; Mismatches 50; Indels 53; Gaps 6;

Qy 90 DLFCFLKSPKSKWAYL-----QVSKHLN-----NTKLSWNEDGTIH 127
Db 47 DAFPEIKSLPPKLLWLYRLFMPSFSQRAKEYIOKHANFEDIIDAQGNLFPFSKEE----- 101

Qy 128 GLIYQDGNLIVPGGLYFIVCQLQFLVQ-----CSNHSVDLTQLLLNSKIKKQTLVTY 181
Db 102 --LKENGTLIVRSVGLYAPHQFOELVQKTNLWLSGNNVFKLLRLKIKKQKN----- 155

Qy 182 CSEGVQSKNIYQNLQFLHYLQVNSTISVRVDNFOYV 219
Db 156 -----QN---YLLSFQKADGIILINSDELAYV 179

RESULT 5
Q9WIS1 PRELIMINARY; PRT; 847 AA.
AC Q9WIS1;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE ENVELOPE GLYCOPROTEIN PRECURSOR, GP160.
OS Human immunodeficiency virus type 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97NOGIL3;
RA Jonassen T.O.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=97NOGIL3;
RX MEDLINE=20092438; PubMed=10628916;
RA Jonassen T.O., Grinde B., Asjo B., Hasle G., Hungnes O.;
RT "Inter-subtype recombinant HIV-1 involving HIV-MAL-like and subtype H-
RT like sequence in four Norwegian cases.";
RL AIDS Res. Hum. Retroviruses 16:49-58(2000).
DR EMBL: AJ237565; CAB39923.2; -
DR InterPro: IPR000328; -
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
SQ SEQUENCE 847 AA; 95496 MW; E8770E4691304EB6 CRC64;

Query Match 7.2%; Score 89.5; DB 14; Length 847;
Best Local Similarity 20.9%; Pred. No. 3;
Matches 37; Conservative 37; Mismatches 56; Indels 47; Gaps 8;

Qy 71 DSTPNTTEKAPLKGNCSEDLCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLI 130
Db 138 DTNTNTSIQPSQNSCNFNVTAIRDKQKVHALYRV-----DLVSDNDNTQYRLI 193

Qy 131 YQDGNLIVQ-----FPGLYFIV-----CQLQFLVQCSNHSVD- 162
Db 194 NCNTSVITQACPKVTFEPIPIHYCAPAGFAILKCNKNTFSGTGPCKNVSTVQCT-HG1KP 252
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Qy 163 -LTQLLLNSKIKKQTLVTVCESGVQSKNIYQNLQFLHY---LQVNSTISVRVDN 215
Db 253 VVSTOLLNGSLAEKVI-----IRSKNTIDNTKNIIVHFNESVOINCT---RIAN 299

RESULT 6
Q9WV90 PRELIMINARY; PRT; 169 AA.
AC Q9WV90;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE FAS LIGAND (FRAGMENT).
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Scuridae; Sciurinae;
OX Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEALTHY LIVER;
RA Hodgson P.D., Grant M.D., Michalak T.I.;
RT "Perforin and Fas/Fas ligand-mediated cytotoxicity in acute and
RT chronic woodchuck viral hepatitis.";
RL Clin. Exp. Immunol. 0:0-0(1999).
DR EMBL: AF152368; AAD38387.1; -
DR InterPro: IPR000478; -
DR Pfam: PF00229; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS00049; TNF_2; 1.
DR SMART: SM00207; TNF; 1.
FT NON_TER 1
FT NON_TER 169
SQ SEQUENCE 169 AA; 19274 MW; FDE395B014717B6B CRC64;

Query Match 7.1%; Score 89; DB 11; Length 169;
Best Local Similarity 24.1%; Pred. No. 0.61;
Matches 33; Conservative 24; Mismatches 42; Indels 38; Gaps 7;

Qy 97 STPSKKS---WAYLQVSKHLNNTKLSWNED---GTIHLIYQDGNLIVPGGLYFIVCQ 149
Db 32 SSPDKALRRRAHLTKGPNSSPLEWETYGISLVYQKGLVINDTGLYFVYSK 91

Qy 150 LQFLVQ-CSN---HSVDLTQLLLNSK-----IKKQTLVTVCESG----- 185
Db 92 IYFRQSCNNQPLSHKV-----YVKNKYPQDLVLMEGKMNCTTGQWARRSSYLGAVF 146

Qy 186 --VOSKNIYQNLQFL 200
Db 147 NFTSNDHLVNVNSEL 163

RESULT 7
Q28320 PRELIMINARY; PRT; 234 AA.
AC Q28320;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TNF-ALPHA.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA Takakura H., Mori Y., Tatsumi M.;
RT "Molecular cloning of caprine TNF-alpha cDNA and its expression in
RT E.coli and insect cells.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
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DR EMBL; D86587; BAA13130.1; -
DR HSSP; P01375; 47SV.
DR InterPro; IPR000478; -
DR InterPro; IPR003636; -
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PRO1234; TNECROSISFCT.
DR PRODOM; PD00212; -; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS0049; TNF_2; 1.
DR SMART; SM00207; TNF; 1.
SQ SEQUENCE 234 AA; 25519 MW; 9768E33BBABB041 CRC64;

Query Match 7.1%; Score 88; DB 6; Length 234;
Best Local Similarity 24.1%; Pred. No. 1.1;
Matches 48; Conservative 38; Mismatches 89; Indels 24; Gaps 8;

Qy 41 SRSFYLTALVCLVAVAILVIVOKDSTPNTEKAPLKGNCSEDLFTCTKST-- 98
Db 27 SRSWCLSLFSF--LLVAGATTFLCLHFGVIGPQREEQSP-AGPSFNRLPLVQTLRSSQ 83
Qy 99 -PSKSWAYLQVSKHLNNTKLSWNEGT-----IHGLIQDGNLIYQFGLYIVCOLQFL 153
Db 84 ASSNKPVAHV-VANISAPQLRWGSDYANALKANGVELKDNQLVPTDGLYLIYSQVLER 142
Qy 154 VQ-CSNHSVDLTQLLINSIKKQTLVTVCES-----GVQSKNIYQNLISQFLH 201
Db 143 GHGCPSTPLFT-HTISRIAYSTQKVNLSAISKPHRETPEGAERKWPYEPYQGGVF 201
Qy 202 YLQNSTISVRVDFQYVD 220
Db 202 QLKGDRLSAEINOPEYLD 220

RESULT 8
Qy Q9M9B0 PRELIMINARY; PRT; 896 AA.
AC Q9M9B0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE F27J15.13.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kim C., Altafi H., Bei Q., Chin C., Chlou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu S., Mukharsky N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F27J15 from chromosome
RT I.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AC016041; AAF69701.1; -
DR InterPro; IPR000719; -
DR InterPro; IPR001245; -
DR InterPro; IPR001611; -
DR InterPro; IPR002290; -
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00560; LRR; 3.
DR PRINTS; PR00019; LEURICHRPT.
DR PRINTS; PR00109; TYRKINASE.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR SMART; SM00220; S_TKC; 1.
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KW ATP-binding; Serine/threonine-protein kinase; Transferase;
KW Tyrosine-protein kinase.
SQ SEQUENCE 896 AA; 99724 MW; A24500615125A15C CRC64;

Query Match 7.0%; Score 87.5; DB 10; Length 896;
Best Local Similarity 21.4%; Pred. No. 5;
Matches 43; Conservative 42; Mismatches 59; Indels 57; Gaps 11;

Qy 9 GSGCAPSPDPAMQVQPGSVASPRSTRPWRSTSRSPYLSTTALVCLVAVAILVIVQ 68
Db 502 GPCGN-----KPGEGHPKRSI-----IVPVSSVALITALIA-AULVFLVLR 543
Qy 69 KDSSTNTTEKAPLKGNCSEDLFTCTKSTP-----SKSWAYLQVSKHLNNTKLSWNEG 124
Db 544 KKN--PSRSK-----ENGRTSR-----SSEPRTTKKKKTYVEVTENFRSVLGGG 591
Qy 125 THGLIYQDGNLIYQFGLYIVCOLQFLVQCSNHS-----VDLTQLLINSIKK 175
Db 592 --FGMYVHG-----YVNGREQVAVKVLSHASKHGKQKAEVELLRVHHK-NL 637
Qy 176 QTLVTVCSGVSQSKNIYQNLIS 196
Db 638 VSLVGCEKGEKELALVYEMA 658

RESULT 9
Qy Q96216 PRELIMINARY; PRT; 2013 AA.
AC Q96216;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE PREDICTED MEMBRANE ASSOCIATED PROTEIN.
GN F80615C.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RA Gardner M.J., Tettelin H., Carucci D.J., Cummings L.M., Aravind L.,
RA Koonin E.V., Shalloom S., Mason T., Yu K., Fujii C., Pederson J.,
RA Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Perlea M.,
RA Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
RA Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Science 282:1126-1132(1998).
DR EMBL; AB001406; AAC71912.1; -
SQ SEQUENCE 2013 AA; 243596 MW; 7AD1F050E79C8731 CRC64;

Query Match 7.0%; Score 87; DB 5; Length 2013;
Best Local Similarity 23.9%; Pred. No. 13;
Matches 34; Conservative 31; Mismatches 49; Indels 28; Gaps 7;

Qy 88 SEDLFTCTLKSTPSKSWAYLQVSKHLNNTKLSWNEGTTHGLIYQDGNLIYQFGLYFIV 147
Db 16 SDNIFCLKD-----GYICFMNLLN-----NEKKYLYITCSQDEGYAQY---YFDV 59
Qy 148 COLQFLVQCSNHSVDLTQLLI-----NSIKKQTLVTVCSGVSQSKNIYQNLISQFL-- 200
Db 60 VKCRYEKKEEDCNKNTINIMLQENKNIKETCYI---KNVVTNKIYHTL--FLVINK 114
Qy 201 HYLQVNSTISVRVDFQYVDN 222
Db 115 HYHNILCSLSFENNSFEILNTN 136

RESULT 10
Qy Q9ERG6 PRELIMINARY; PRT; 217 AA.
ID Q9ERG6
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Db 970 SVAPPROENPIKIDNEALLRROFFPIFHSAANKVYVAVPPIDQSOYMISSSIVOEIKV 1029
QY 59 VAILVLVQKKD---STNTTEKAPLKGNCSEDLFTCLKSTPSKKS-----WAYLOV 109
Db 1030 TPI--DOIIPNDMLKSPGPGLSAKKKDLTKWMETTIKSISENESSTDMTIWQLEM 1087
QY 110 SKHLNNTKLSWNEGTIHLIYODGNLIV-----QFPGLY--FIVCQLQFL--VQ 155
Db 1088 KL---NDKVNWK---NISKLLYNSDELLMVLQSOPFGNDMPINAYRLDINCOMRVLAFLQ 1141
QY 156 CSNHSV-----DLTQLLINSIKKOTLVTV-----ESGVOSKNYQNSOFLHL 201
Db 1142 TGNHDEALRLALSKRDAYATALLVGLSLMGKDRWSEVIQKLYEFTAGPNDOKELAFLLL 1201
QY 202 YLOV---NSTISVR 212
Db 1202 IFOVFVGNKMAIK 1215

RESULT 12
Q06629 PRELIMINARY; PRT; 674 AA.
AC Q06629;
DT 01-NOV-1996 (TremBLrel. 01, Created)
DT 01-NOV-1996 (TremBLrel. 01, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE SIMILARITY TO STREPTOCOCCUS PROTEIN V.
GN D9740.10 OR PLO2.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favell A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
RA Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
RA Taich A., Travaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,
RA Wilson R., Waterston R.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Ding H.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Waterston R.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Jia Y., Cherry J.M.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U28374; AAB64731.1; -.
DR SGD; S0002703; PLO2.
DR InterPro; IPR000255; -.
DR InterPro; IPR001871; -.
DR PROSITE; PS00036; BZIP_BASIC; UNKNOWN_1.
DR PROSITE; PS00012; PHOSPHATETHEINE; UNKNOWN_1.
SQ SEQUENCE 674 AA; 77059 MW; CE768CBCC84CCD97 CRC64;

Query Match 6.9%; Score 86; DB 3; Length 674;
Best Local Similarity 25.0%; Pred. NO. 5.1;
Matches 40; Conservative 30; Mismatches 60; Indels 30; Gaps 9;

QY 70 KDSTPNTTEKAPLKGNCSE-----EDFCTLKSTPSKK-----SWAYLOVSKHLNNTK- 117
|||||
Db 192 KGPNSVSSSSNSNSTSYTGSKDDYDYSVKRLNKRKINTDDWLFATTKHLKHQDY 251
|||||
QY 118 LSWNEEDGTIHLIYODGNLIVQFPGLYFI-----VCQLQLVQCSNHSVDLTQLLIN 170
```

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|||||
Db 252 LLANYD--IDMIISDFPMLEVELPALQVIRNANKRPIIKLLVQ---NSPD---HYLLD 303
QY 171 SKIKQTLVT--VCESG-VQSKNYIQNSQLLHLHVQNS 207
Db 304 SEIKNSVKSHLSNNGHVDSDQYEIEKSSLLYFLQARN 343

RESULT 13
Q9FID8 PRELIMINARY; PRT; 873 AA.
ID Q9FID8;
AC Q9FID8;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE RECEPTOR-LIKE PROTEIN KINASE.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=COLUMBIA;
RC MEDLINE=99156233; PubMed=10048488;
RA Asamizu E., Sato S., Kaneko T., Nakamura Y., Kotani H., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. VIII.
RT Sequence features of the regions of 1,081,958 bp covered by seventeen
RT physically assigned P1 and TAC clones."
RL DNA Res. 5:379-391(1998).
DR EMBL; AB016892; BAB10824.1; -.
KW Kinase.
SQ SEQUENCE 873 AA; 97164 MW; B2879DE5BC7337A7 CRC64;

Query Match 6.9%; Score 85.5; DB 10; Length 873;
Best Local Similarity 23.5%; Pred. NO. 7.5;
Matches 47; Conservative 43; Mismatches 79; Indels 31; Gaps 11;

QY 9 GSCGAPDPAMQVQGSVAPWRSTSRYSYFLSTALVCLVAVAI---ILV 64
|||||
Db 410 GNLGPNPDPL--VSPDLI--PNRAT-PRIRKKNKSHLPITLAVGSLVLA MFVGVLV 464
|||||
QY 65 LVQKKDSTPTTEK-APLKGNCSEDLFTCLKSTPSK--KSWAYLOVSKHLNNTKLSWN 121
|||||
Db 465 IMKKKKSKSTNSWCPLPHGTDSTNT-RPAKSLPADLCRRFSIFEIKSATNDF----- 518
|||||
QY 122 EDGTIHL-----IYQDGNLIVQFPGLYFIVCQLQLVQCSNHSVDLTQLLINSIKKQ 176
|||||
Db 519 EDKLIIGVGFGSVYKG-----QIDGGATLVAVKRLKLEITSNQAKFEFETEMLSKLRHV 573
|||||
QY 177 TLVTV---CESGVOSKNYQ 193
|||||
Db 574 HLVSILGYCEDNEMLVAYE 593

RESULT 14
Q9FKU2 PRELIMINARY; PRT; 283 AA.
ID Q9FKU2;
AC Q9FKU2;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE GENOMIC DNA, CHROMOSOME 5, P1 CLONE:MDA7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=COLUMBIA;
```



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2001, 10:23:15 ; Search time 19.38 Seconds  
(without alignments)  
422.449 Million cell updates/sec

Title: US-09-628-126-6  
Perfect score: 1246  
Sequence: 1 MPEGLQAGSCGAPSPDPAM.....DTNFFPLDNLVSLYSSSD 239

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1246	100.0	239	1 TNF8_MOUSE	P32972 mus musculus
2	860.5	69.1	234	1 TNF8_HUMAN	P32971 homo sapien
3	123	9.9	279	1 FASL_MOUSE	P41047 mus musculus
4	102	8.2	278	1 FASL_RAT	P36940 rattus norv
5	91	7.3	309	1 41BL_MOUSE	P41274 mus musculus
6	89.5	7.2	235	1 TNFA_PERLE	P36939 peromyscus
7	87	7.0	281	1 FASL_HUMAN	P48023 homo sapien
8	86.5	6.9	233	1 TNFA_MACMU	P48094 macaca mula
9	86.5	6.9	2194	1 SC16_YEAST	P48415 saccharomyc
10	85	6.8	291	1 TN10_MOUSE	P50592 mus musculus
11	84.5	6.8	525	1 C307_DROME	Q9vrm7 drosophila
12	83.5	6.7	201	1 TNFB_MACFU	Q9xt48 macropus eu
13	83.5	6.7	233	1 TNFA_MACFA	P79337 macaca fasc
14	82.5	6.6	233	1 TNFA_PAPHU	O77510 papio hamad
15	82.5	6.6	965	1 APN_MOUSE	P97449 mus musculus
16	82.5	6.6	1078	1 S24A_HUMAN	O95486 homo sapien
17	82	6.6	234	1 TNFA_SHEEP	P23383 ovis aries
18	81.5	6.5	233	1 TNFA_CANFA	P51742 canis famil
19	81	6.5	460	1 ENV_HV123	P12491 human immun
20	80.5	6.5	1376	1 RPOD_ARATH	P56764 arabidopsis
21	79.5	6.4	383	1 COS7_YEAST	Q07788 saccharomyc
22	79	6.3	229	1 TNFA_CEREL	P51743 cercus elap
23	79	6.3	851	1 NUD1_YEAST	P32336 saccharomyc
24	78.5	6.3	234	1 TNFA_HORSE	P29553 equus cabal
25	78.5	6.3	235	1 TNFA_RAT	P16599 rattus norv
26	78.5	6.3	507	1 C392_DROME	P82713 drosophila
27	78.5	6.3	816	1 NEL2_RAT	Q62918 rattus norv
28	78.5	6.3	1150	1 IRR1_YEAST	P40541 saccharomyc
29	78	6.3	396	1 BMP2_HUMAN	P13643 homo sapien
30	78	6.3	856	1 ENV_HV1MN	P05877 human immun
31	77.5	6.2	178	1 IL10_MACFA	P79338 macaca fasc
32	77.5	6.2	463	1 YKN3_YEAST	P36066 saccharomyc
33	77.5	6.2	1583	1 MIS4_SCHPO	Q09725 schizosacch

#### ALIGNMENTS

```
RESULT 1
TNF8_MOUSE
ID TNF8_MOUSE STANDARD; PRT; 239 AA.
AC P32972;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD30 LIGAND (CD30-L).
GN TNFSF8 OR CD30LG OR CD30L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=T-cell;
RX MEDLINE=93313964; Pubmed=8391931;
RA Smith C.A., Gruess H.-J., Davis T., Anderson D., Farrah T.,
RA Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA Grabstein K.H., Gliniak B., McAllister I.B., Fanslow W., Alderson M.,
RA Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.;
RT "CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
RT ligand defines an emerging family of cytokines with homology to
TNF.";
RL Cell 73:1349-1360(1993).
CC -!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
CC T CELLS.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC EMBL; L09754; AAA74595.1; -.
CC PIR; B40710; B40710.
CC MGD; MGI:88328; Tnf8.
CC InterPro: IPR000478; -.
CC Pfam; PF00229; TNF; 1.
CC PROSITE; PS00251; TNF_1; 1.
CC PROSITE; PS50049; TNF_2; 1.
CC Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
CC DOMAIN 1 43 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 44 67 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
CC DOMAIN 68 239 EXTRACELLULAR (POTENTIAL).
CC CARBOHYD 75 75 N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOHYD 86 86 N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOHYD 114 114 N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOHYD 158 158 N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOHYD 194 194 N-LINKED (GLCNAC...) (POTENTIAL).
CC CARBOHYD 206 206 N-LINKED (GLCNAC...) (POTENTIAL).
CC SEQUENCE 239 AA; 26519 MW; 29003157DDA25159 CRC64;
```

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Query Match 100.0%; Score 1246; DB 1; Length 239;
Best Local Similarity 100.0%; Pred. No. 9.3e-107;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPGLQAGSGCAPSPDPAMQVQPGSVASPMRSTRPWRSTRSYFYLSYFVLTALVCLVAV 60
D 1 MEPGLQAGSGCAPSPDPAMQVQPGSVASPMRSTRPWRSTRSYFYLSYFVLTALVCLVAV 60
QY 61 IILVLVQKDSPTNTTEKAPLKGNCSEDLCTLKSTPSKSWAYLOVSKHLNNTKLSW 120
D 61 IILVLVQKDSPTNTTEKAPLKGNCSEDLCTLKSTPSKSWAYLOVSKHLNNTKLSW 120
QY 121 NEDGTIHLIYQDGNLIYQVQGLYFIVQQLQFLVQCSNHSVDLTQLLINSIKKQTLV 180
D 121 NEDGTIHLIYQDGNLIYQVQGLYFIVQQLQFLVQCSNHSVDLTQLLINSIKKQTLV 180
QY 181 VCESGVQSKNIYQNSQFLHLYLQVNSTISVRDNFYQVYDNTFPDLNVLVSFLYSSD 239
D 181 VCESGVQSKNIYQNSQFLHLYLQVNSTISVRDNFYQVYDNTFPDLNVLVSFLYSSD 239

RESULT 2
TNF8_HUMAN
ID TNF8_HUMAN STANDARD; PRT; 234 AA.
AC P32971;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE CD30 LIGAND (CD30-L) (CD153 ANTIGEN).
GN TNFSF8 OR CD30LG OR CD30L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RX MEDLINE=93313964; Pubmed=8391931;
RA Smith C.A., Guess H.-J., Davis T., Anderson D., Farrah T.,
RA Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA Grabstein K.H., Gliniak B., McAllister I.B., Fanslow W., Alderson M.,
RA Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.;
RT "CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
RT ligand defines an emerging family of cytokines with homology to
RT TNF."
RL Cell 73:1349-1360(1993).
CC -!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
CC T CELLS.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD153 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd153.htm".
CC -----
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CC -----
CC EMBL; L09753; AAA74594.1; -
CC PIR; A0710; A40710.
CC MIM; 603875; -
CC InterPro; IPR000478; -
CC Pfam; PF00229; TNF; 1.
CC PROSITE; PS00251; TNF.1; 1.
CC PROSITE; PS50049; TNF.2; 1.
CC Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
KW DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT SIGNAL 38 62 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT FT 63 234 EXTRACELLULAR (POTENTIAL).
```

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FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 109 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 201 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 234 AA; 26017 MW; C653615682305B1B CRC64;

Query Match 69.1%; Score 860.5; DB 1; Length 234;
Best Local Similarity 69.6%; Pred. No. 1.5e-71;
Matches 167; Conservative 28; Mismatches 38; Indels 7; Gaps 2;

QY 1 MEPGLQAGSGCAPSPDPAMQVQPGSVASPMRSTRPWRSTRSYFYLSYFVLTALVCLVAV 59
D 1 MDPGLQALNGMAPPDGTAMHVPAAGSVAS-----HLGTTSRSYFYLTATLCLCLVFTV 54
QY 60 AITLVVQKDSPTNTTEKAPLKGNCSEDLCTLKSTPSKSWAYLOVSKHLNNTKLS 119
D 60 AITLVVQKDSPTNTTEKAPLKGNCSEDLCTLKSTPSKSWAYLOVSKHLNNTKLS 119
QY 120 WNEGTIHLIYQDGNLIYQVQGLYFIVQQLQFLVQCSNHSVDLTQLLINSIKKQTLV 179
D 120 WNEGTIHLIYQDGNLIYQVQGLYFIVQQLQFLVQCSNHSVDLTQLLINSIKKQTLV 179
QY 115 WNKDGIHLGVYQDGNLIYQVQGLYFIVQQLQFLVQCPNNSVDLKLKLELLINKHKQALV 174
D 115 WNKDGIHLGVYQDGNLIYQVQGLYFIVQQLQFLVQCPNNSVDLKLKLELLINKHKQALV 174
QY 180 TVCESGVQSKNIYQNSQFLHLYLQVNSTISVRDNFYQVYDNTFPDLNVLVSFLYSSD 239
D 175 TVCESGMQTRHVYQNSQFLHLYLQVNSTISVRDNFYQVYDNTFPDLNVLVSFLYSSD 234

RESULT 3
FASL_MOUSE
ID FASL_MOUSE STANDARD; PRT; 279 AA.
AC P41047; O61217; O9R1F2;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FAS ANTIGEN LIGAND.
GN TNFSF6 OR APTILG1 OR FASL OR GLD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RX MEDLINE=94185175; Pubmed=7511063;
RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
RA Suda T., Nagata S.;
RT "Generalized lymphoproliferative disease in mice, caused by a point
RT mutation in the Fas ligand."
RL Cell 76:969-976(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
RC STRAIN=C57BL/6;
RX MEDLINE=95388076; Pubmed=7544870;
RA Peitsch M.J., Tschoopp J.J.;
RT "Comparative molecular modelling of the Fas-ligand and other members
RT of the TNF family."
RL Mol. Immunol. 32:761-772(1995).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=95196085; Pubmed=7889405;
RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a
RT TNF family gene cluster."
RL Immunity 1:131-136(1994).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RC STRAIN=BALB/C;
RA Fenner M.H., Shioda T., Isselbacher K.J.;
RT "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in
RT two amino acids."
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
```

FN  
RP SEQUENCE FROM N.A. (ISOFORM FASLS).  
RC STRAIN=C3H; TISSUE=Spleen;  
RX MEDLINE=20021694; PubMed=10552956;  
RA Ayroldi E., D'Adamo F., Zollo O., Agostini M., Moraca R.,  
RA Cannarile L., Migliorati G., Delfino D.V., Riccardi C.;  
RT "Cloning and expression of a short Fas ligand: A new alternatively  
RT spliced product of the mouse Fas ligand gene.";  
RL Blood 94:3456-3467(1999).  
RN [6]  
RX CHARACTERIZATION OF VARIANT GLD.  
RX MEDLINE=96091792; PubMed=7495745;  
RA Hahne M., Peitsch M.C., Irmeler M., Schroeter M., Lowin B.,  
RA Rousseau M., Bron C., Renno F., French L., Tschopp J.;  
RT "Characterization of the non-functional Fas ligand of gld mice.";  
RL Int. Immunol. 7:1381-1386(1995).  
CC -!- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT  
CC TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN  
CC CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.  
CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF  
CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE  
CC T CELLS, OR BOTH.  
CC -!- SUBUNIT: HOMOTRIMER (PROBABLE).  
CC -!- SUBCELLULAR LOCATION: ISOFORM FASL IS A TYPE II MEMBRANE PROTEIN.  
CC ISOFORM FASLS IS SOLUBLE.  
CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; FASL (SHOWN HERE) AND FASLS; ARE  
CC PRODUCED BY ALTERNATIVE SPLICING. ISOFORM FASL MEDIATES APOPTOSIS  
CC WHILE ISOFORM FASLS PREVENTS APOPTOSIS INDUCED BY FAS/FASL  
CC INTERACTION.  
CC -!- DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERALIZED  
CC LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DISEASE  
CC RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION.  
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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CC -----  
CC EMBL: U06948; AAA17800.1; -  
CC EMBL: U10984; AAA19778.1; -  
CC EMBL: S76752; AAB33780.1; -  
CC EMBL: U58995; AAB02915.1; -  
CC EMBL: AF119335; AAD52106.1; -  
CC HSP: P01375; 2TUN.  
CC MGD: MGI:92255; Fasl.  
CC InterPro: IPR000478; -  
CC Pfam: PF00229; TNF; 1.  
CC PROSITE: PS00251; TNF\_1; 1.  
CC PROSITE: PS0049; TNF\_2; 1.  
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis;  
KW Disease mutation; Alternative splicing.  
FT DOMAIN 1 78 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 79 100 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
FT DOMAIN 101 279 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 4 69 PRO-RICH.  
FT DOMAIN 45 51 POLY-PRO.  
FT DISULFID 200 231 BY SIMILARITY.  
FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARSPLIC 1 210 MISSING (IN ISOFORM FASLS).  
FT VARIANT 184 184 T -> A (IN STRAIN BALB/C).  
FT VARIANT 218 218 E -> G (IN STRAIN BALB/C).  
FT VARIANT 273 273 F -> L (IN GLD; ABOLISHES BINDING OF FASL  
FT TO ITS RECEPTOR).  
SQ SEQUENCE 279 AA; 31442 MW; 37972E2728E0A1CA CRC64;

Query Match 9.9%; Score 123; DB 1; Length 279;  
Best Local Similarity 22.5%; Pred. No. 0.00043;  
Matches 55; Conservative 43; Mismatches 96; Indels 50; Gaps 11;  
QY 10 SCG-----APSPDPAMQVPGSVASPRWSTPRWSTRS-----YFVLSTALV 53  
DB 34 SCGPRGPQRRPPPPPPVSPPLPPPLPLPLPLKDKKDHNTNMLPVPVFFVVLVALV 93  
QY 54 CLVAVAILVLVQKDSPTNTEKAPLGGKNCSEDLFTLKSTPSKK-----SWAYLQV 109  
DB 94 GM--GLGMVQLPHLQKELAELEFTNQSLKVSFEKQI--ANPSTPEKKEPRVAHLTG 149  
QY 110 SKHLNNTKLSWNE--GT--IHGLIYQDGNLIVQFGLFIVCOLQPLVQ--CSNHSVDLTL 165  
DB 150 NPHSISIPLEWEDTYGTALISGKVLGGLVNETGLTFVYKSVYFRGSCNQNPLNHKV 209  
QY 166 OLLINSK-----IKQTLVTVCESG-----VQSKNIYONLSQFLLHLQ 204  
DB 210 YMR-NSKYPEDIVLMEEKRLNYCTTGQIWAHSSYLGAVENTLTSADHLVYNISQLSINF 268  
QY 205 VNST 208  
DB 269 ESKT 272  
RESULT 4  
FASL\_RAT  
ID FASL\_RAT STANDARD; PRT; 278 AA.  
AC P36940;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE FAS ANTIGEN LIGAND.  
GN TNFSF6 OR APTLIG1 OR FASL.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
ON NCBI\_TaxID=10116;  
RX SEQUENCE FROM N.A.  
RX MEDLINE=94084792; PubMed=7505205;  
RA Suda T., Takahashi T., Golstein P., Nagata S.;  
RT "Molecular cloning and expression of the Fas ligand, a novel member  
RL of the tumor necrosis factor family.";  
RL Cell 75:1169-1178(1993).  
CC -!- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT  
CC TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN  
CC CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.  
CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF  
CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE  
CC T CELLS, OR BOTH.  
CC -!- SUBUNIT: HOMOTRIMER (PROBABLE).  
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED  
CC INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL  
CC SURFACE.  
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND  
CC THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES,  
CC KIDNEY AND LUNG.  
CC -!- INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.  
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
CC EMBL: U03470; AAC52129.1; -  
CC InterPro: IPR000478; -  
CC Pfam: PF00229; TNF; 1.  
CC PROSITE: PS00251; TNF\_1; 1.



```
CC  EXTRACELLULAR SOLUBLE FORM.
CC  -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC  PROTEOLYTIC PROCESSING.
CC  -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC  CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC  AND MALNUTRITION.
CC  -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; M59233; AAA40596.1; -
DR  HSP; P01375; 2TUN.
DR  InterPro; IPR000478; -
DR  InterPro; IPR002959; -
DR  Pfam; PF00229; TNF; 1.
DR  PRINTS; PR01234; TNECROSISFCT.
DR  PRINTS; PR01235; TNFALPHA.
DR  PROSITE; PS00251; TNF_1; 1.
DR  PROSITE; PS50049; TNF_2; 1.
DR  Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
KW  PROPEP 1 79 BY SIMILARITY.
FT  CHAIN 80 235 TUMOR NECROSIS FACTOR.
FT  TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT  DISULFID 148 179 BY SIMILARITY.
FT  CARBOHYD 86 86 N-LINKED (GLCNAC...) (POTENTIAL).
SQ  SEQUENCE 235 AA; 25822 MW; 235A5CFC9F9AC624 CRC64;

Query Match 7.2%; Score 89.5; DB 1; Length 235;
Best Local Similarity 23.6%; Pred. No. 0.4;
Matches 53; Conservative 39; Mismatches 94; Indels 39; Gaps 11;

QY 19 AMQVQGSVASPRWRTPMRSTRSYFLS-TTALVCLVAVAILLVLVVQKKDSTPTNT 77
DB 13 ABEALPKKAWGPQNSRCLCLSLFSLVAGATFLCLL-----NFGVIGPQREKFPN-- 66

QY 78 EKAPLKGNCSEDLFTLKTST---PSKKSWAYLQVSKHLNLTLSWEDGT-----IHGLI 130
DB 67 -NLPIIGSMAQT---LTLRSSQNSSDPKVAHV-VANHQVDEQLWLSRGANALLANGMD 121

QY 131 YDGNLIVQPGGLYFVLCQLQFLVQ-CSN-----HSVD-----LTQLLLNSIKK 175
DB 122 LKDNQLVLPADGLYLYVSQVLFKQGGCSSVLLTHTVSRFAVSVDKVNLLSAIKSPCKP 181

QY 176 QTLVTVCSGVSQSKNIYQNLISQFLHLYLVNSTISVRVDNFQYVD 220
DB 182 ET-----PEGSELKPWEPIYLGVSFQLEKGDRLSAEVLNPKYLD 221

RESULT 7
FASL_HUMAN STANDARD; PRT; 281 AA.
AC P48023;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL).
GN TNFSF6 OR APTL1G1 OR FASL.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95105731; PubMed=7528780;
RA Alderson M.;
RT "Fas ligand mediates activation-induced cell death in human T
```

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RT lymphocytes."
RL J. Exp. Med. 181:71-77(1995).
[2]
RN SEQUENCE FROM N.A.
RX MEDLINE=95127560; PubMed=7826947;
RA Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
RA "Human Fas ligand: gene structure, chromosomal location and species
RA specificity."
RT Int. Immunol. 6:1567-1574(1994).
[3]
RN SEQUENCE FROM N.A.
RX Schaeublein C.E., Poehmann R., Philippsen P., Eibel H.;
RA Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
[4]
RN SEQUENCE FROM N.A.
RX MEDLINE=95071350; PubMed=7980502;
RA Mita E., Hayashi N., Iio S., Takehara T., Hijoka T., Kasahara A.;
RA Fusamoto H., Kamada T.;
RT "Role of Fas ligand in apoptosis induced by hepatitis C virus
RT infection."
RL Biochem. Biophys. Res. Commun. 204:468-474(1994).
[5]
RN SEQUENCE FROM N.A.
RX Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
[6]
RN SEQUENCE OF 1-10 FROM N.A.
RP TISSUB-Blood;
RA Matsumura M., Nakanishi Y., Ohba Y.;
RA Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
CC TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
CC CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
CC T CELLS, OR BOTH.
CC -!- SUBUNIT: HOMOTRIMER (PROBABLE).
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
CC INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
CC SURFACE.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
DR  EMBL; X89102; CAA61474.1; -
DR  EMBL; U08137; AAC50071.1; -
DR  EMBL; U11821; AAC50124.1; -
DR  EMBL; D38122; BAA07320.1; -
DR  EMBL; Z96050; CAB09424.1; -
DR  EMBL; AB013303; BAA32542.1; -
DR  HSP; P01375; 2TUN.
DR  MIM; 134638; -
DR  InterPro; IPR000478; -
DR  Pfam; PF00229; TNF; 1.
DR  PROSITE; PS00251; TNF_1; 1.
DR  PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis.
FT DOMAIN 1 80 CYTOPLASMIC (POTENTIAL)
FT TRANSMEM 81 102 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 103 281 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 4 70 PRO-RICH.
FT DOMAIN 45 65 POLY-PRO.
FT DISULFID 202 233 BY SIMILARITY.
FT CARBOHYD 184 184 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 250 250 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 281 AA; 31485 MW; A8A6EB358246E9BB CRC64;
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Query Match	7.0%	Score 87:	DB 1;	Length 281;
Best Local Similarity	20.3%	Pred. No. 0.84;		
Matches 50;	Conservative 38;	Mismatches 88;	Indels 70;	Gaps 11;

  

QY	14	PSPPAMQVPGSVASVWRSRTRPRWRSRYSFYLSLTALVCLVAVAILLVV-----	67
DB	48	PPPPPLPPPPPPPPPLPPLPPLPKKRG-----HSTGL-CLLVYFMVVALVGLGLGM	101
QY	68	-----OKKDSPTNTEKAPLKGNCSEDLFCTLKSTPSKSW--AYLQVSK	111
DB	102	FQFLHQLKELAEALRETSQMTASSLEKQIGHPS-----PPEKKELKRVAAHLTGKS	153
QY	112	HLNNTKLSWNEGTI---HGLIYDGNLIVQFPGLYTIVCQLQFLVQ-CSN---HSVDL	163
DB	154	NSRSMPLWEEDTYGIVLLSGVKYKKGGLVNETGLGYFYYSKVYFGQSCNPLSHRV--	211
QY	164	TLQLLINSK-----IKQFLVTVCESG-----VOSKNIYNLQSFLHY	202
DB	212	---YMRNSKYQDILVMMEGKMMSYCTTCQWARSYLGAVENLTSAHLYVNVSELSLVN	268
QY	203	LOYNST 208	
DB	269	FESQT 274	

  

RESULT	8
TNFA_MACMU	STANDARD; PRT; 233 AA.
ID	TNFA_MACMU
AC	P48094;
DT	01-FEB-1996 (Rel. 33, Created)
DT	01-FEB-1996 (Rel. 33, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN	TNF OR TNFA.
OS	Macaca mulatta (Rhesus macaque).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC	Cercopithecoidea; Macaca.
OX	NCBI_TaxID=9544;
RN	[1]
RP	SEQUENCE FROM N.A.
RP	MEDLINE=96003435; PubMed=7561102;
RA	Villinger F.J., Brar S.S., Wayne A.E., Chikkala N., Ansari A.A.;
RT	"Comparative sequence analysis of cytokine genes from human and
RT	nonhuman primates";
RL	J. Immunol. 155:3946-3954(1995).
CC	-!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
CC	WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CC	CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC	CACHECTIN, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC	OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC	CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC	CONDITIONS.
CC	-!- SUBUNIT: HOMOTRIMER.
CC	-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC	EXTRACELLULAR SOLUBLE FORM.
CC	-!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC	PROTEOLYTIC PROCESSING.
CC	-!- DISEASE: CACHECTIN ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC	CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC	AND MALNUTRITION.
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC	-----
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----

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CC -----
DR EMBL; U23819; AAC49088.1; -.
KW SGI; S0006006; SEC10.
FT L->S: IN SEC16-4; TS ACCUMULATION OF ER
FT MUTAGEN 1058 1058 MEMBRANES.
FT MUTAGEN 1083 1083 L->P: IN SEC16-3; TS ACCUMULATION OF ER
FT MUTAGEN 1088 1088 L->P: IN SEC16-2; TS ACCUMULATION OF ER
FT MUTAGEN 1230 1230 W->R: IN SEC16-1; TS ACCUMULATION OF ER
FT SEQUENCE 2194 AA; 241613 MW; BB1E02D2AD4683E3 CRC64;
SQ

Query Match 6.9%; Score 86.5; DB 1; Length 2194;
Best Local Similarity 20.9%; Pred. No. 12;
Matches 53; Conservative 39; Mismatches 87; Indels 75; Gaps 13;

QY 26 SVASPRWSTRP-----WRSTSRSYF-----YLTALVCLVVA 58
DB 969 SVAPPRQENPNKIDNEALLRRQFFIFHWSAANKVVIYVPPIDQSQYMISSIVQEIKV 1028
QY 59 VAILVLVVOKKD---STPNTTEKAPLKGNGCEDLCTLKSTPSKKS-----WAYLOV 109
DB 1029 TPI--DQIKPNMDLKSFPGLGSAKLKKDLTKWETTKISSENESSDWTIMOLLEM 1086
QY 110 SKHLNKLWNEDGTHGLIYODGNLIY-----QFFGLY--FIVCQLQFL--VQ 155
DB 1087 KL---NDKVNKK---NISKLLYNSDELLMYLSQPPNGMDIPNAYRLDINCOMRVLAFLQ 1140
QY 156 CSNHVS-----DLFLQLLNSKIKQTTLTVTC-----ESGVOSKNIYQNLSOFLH 201
DB 1141 TGNHEALRLALSCKRDYATALLVGLSIMGKDRWSEVIQKLYEGFTAGPNDQKELAHFLL 1200
QY 202 YLOV---NSTISVR 212
DB 1201 IFQVEFGNSKMAIK 1214

RESULT 10
TN10_MOUSE
ID TN10_MOUSE STANDARD; PRT; 291 AA.
AC P50592;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 10 (TNF-RELATED
GN APOPTOSIS INDUCING LIGAND) (TRAIL PROTEIN).
OS TNFSF10 OR TRAIL.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96111955; PubMed=8777713;
RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,
RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,
RA Goodwin R.G.;
RT "Identification and characterization of a new member of the TNF
family that induces apoptosis."
RL Immunity 3:673-682(1995).
CC -!- FUNCTION: INDUCES APOPTOSIS.
CC -!- SUBUNIT: HOMOTRIMER (POTENTIAL).
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).
CC -!- TISSUE SPECIFICITY: WIDESPREAD.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
DR EMBL; U37522; AAC52345.1; -.
DR MGD; MGI:107414; Tnfsf10.
DR InterPro; IPR000478; -.
DR Pfam; PF00229; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
KW Cytokine; Transmembrane; Signal-anchor; Apoptosis.
FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 18 38 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 39 291 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 52 52 N-LINKED (GLCNAC...) (POTENTIAL).
FT SEQUENCE 291 AA; 33477 MW; 3FEACAB9FD7D802 CRC64;
SQ

Query Match 6.8%; Score 85; DB 1; Length 291;
Best Local Similarity 21.2%; Pred. No. 1.3;
Matches 51; Conservative 34; Mismatches 94; Indels 62; Gaps 10;

QY 31 WRST-----RPMRSTSRSYFYLTALVCLVVAI-----IIVLVQKSDSTPNTTEK 79
DB 69 WDSIDGELLNRPCLQVAKRLYO-----LIEEVLRTFQDTISTVPERKOLSTP----- 115
QY 80 APLKGGNCSEDLFTLKSTPSKKSWAYLOVSKH---LNNTKLSWNEDGTHG-----LIYQ 132
DB 116 -PLPRGGRPKVAAHITGITRRSSALIPISKDGKTLGQKIESWESSRKGHSFLNHLFR 174
QY 133 DGNLIVOPGLYFIVCQLQFLVQCSNHSVDLTQLLNSKIKQTIV----- 179
DB 175 NGELVIEQGLIYISQTYFRFQ-----EAEDASKMSKDKVTRKQLVQIYIKYTSYDPPI 230
QY 180 -----TVCESGVOSKNIYQNLSOFLHLYOVNSTISVRVDNFQYVDTNFPDLNLSV 232
DB 231 VLMKSARNSCWSRDAEYGLY-SIYQGLFLKKNDRIFSVTNEHLM-----LDQEASF 284
QY 233 F 233
DB 285 F 285

RESULT 11
C307_DROME
ID C307_DROME STANDARD; PRT; 525 AA.
AC Q9VRM7;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROBABLE CYTOCHROME P450 307A1 (EC 1.14.-.-) (CYPCCCVIA1).
GN CYP307A1 OR CG10594.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
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Db 352 IQEIDAIIIEENSRINLLDNAMPYTMATIFEVRLYSST 391

RESULT 12
TNFB_MACEU
ID TNFB_MACEU STANDARD; PRT; 201 AA.
AC Q9XT48;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE LYMPHOTOXIN-ALPHA PRECURSOR (LT-ALPHA) (TNF-BETA).
GN LTA OR TNFB.
OS Macropus eugenii (Tamar wallaby).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Diprotodontia; Macropodidae; Macropus.
OX NCBI_TaxID=9315;
RN [1]
RP SEQUENCE FROM N.A.
RT Harrison G.A., Cooper D.W., Deane E.M.;
RT "CDNA cloning of lymphotoxin alpha (LT-a) from a marsupial, Macropus
RT eugenii."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: LYMPHOTOXIN IS A CYTOKINE PRODUCED BY LYMPHOCYTES WHICH
CC IS CYTOTOXIC FOR A WIDE RANGE OF TUMOR CELLS IN VITRO AND IN VIVO.
CC -!- SUBUNIT: HETEROTRIMER OF EITHER TWO BETA AND ONE ALPHA SUBUNITS
CC OR (LESS PREVALENT) TWO ALPHA AND ONE BETA SUBUNITS.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
CC EMBL; AF119336; AAD41773.1; -
CC InterPro: IPR000478; -
CC InterPro: IPR002960; -
CC Pfam: PF00229; TNF.1.
CC PRINTS; PR01234; TNECROSISFCT.
CC PRINTS; PR01236; TNFBETA.
CC PROSITE; PS00251; TNF_1.
CC PROSITE; PS00049; TNF_2.
CC Cytokine; Glycoprotein; Cytotoxin; Signal.
CC SIGNAL 1 27 BY SIMILARITY.
CC CHAIN 28 201 LYMPHOTOXIN-ALPHA.
CC CARBOHYD 93 93 N-LINKED (GLCNAC..) (POTENTIAL).
CC SEQUENCE 201 AA; 21536 MW; 8C4C371CB5091627 CRC64;

Query Match 6.7%; Score 83.5; DB 1; Length 201;
Best Local Similarity 22.3%; Pred. No. 1.2;
Matches 49; Conservative 36; Mismatches 52; Indels 83; Gaps 14;

QY 47 LSTALVCLVAVAIILVLVVKDSTPNTEKAPLKGNCSEDLFTCLKSTPSKSWAY 106
DB 1 MTSSGVLCLLGALSLQVLL-----OPGAQGAAPNDNSH-----SSAPP---- 42

QY 107 LQVSKHLNNTKLS-----W--NEDGTI--HGLIVQDGNLIVQFP 141
DB 43 -QTAHLSQKSLARETLKPAHLVGDPSVDSTHWRANTDHAFLRHGFSLSNNLSLVPTS 101

QY 142 GLYFIVCOLOFL-VOCS-----NHSVDLTQLLINSKIKKOTLV-----TVCESGV 186
DB 102 GLYFVYSQVVFSGASCSEPTLLYLSHEV-----LLFSSKYQVHVPLLSAQKSV- 155

QY 187 QS---KNIQNLSQL-----HYLQVNSTI 209
DB 156 QGPWMSRVYQ-AGVFLLTQGRDLSTYTDGVSHLLQSPSSV 194

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RESULT 13
TNFA_MACFA STANDARD; PRT; 233 AA.
ID TNFA_MACFA STANDARD; PRT; 233 AA.
AC P79337;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
TNF OR TNFA.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocytes;
RA Tatsumi M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA. IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -!- SUBUNIT: HOMOTRIMER.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AB000513; BAA119131.1; -
CC HSP; P01375; 1TNF.
CC InterPro: IPR000478; -
CC InterPro: IPR002959; -
CC Pfam: PF00229; TNF; 1.
CC PRINTS: PR01234; TNCRSISFCT.
CC PROSITE: PS00251; TNF_1; 1.
CC PROSITE: PS00049; TNF_2; 1.
CC Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
FT PROPEP 1 76 BY SIMILARITY.
FT CHAIN 77 233 TUMOR NECROSIS FACTOR.
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DISULFID 145 177 BY SIMILARITY.
SQ SEQUENCE 233 AA; 25558 MW; 6ABF2C3AB132C217 CRC64;

Query Match 6.7%; Score 83.5; DB 1; Length 233;
Best Local Similarity 23.4%; Pred. No. 1.4;
Matches 51; Conservative 40; Mismatches 100; Indels 27; Gaps 10;

Qy 19 AMQVPGSVASPRWTRPRWRSYFLSTTA-LVCLVVAIVAILLVVQKKDSTPNNT 77
Dy 13 ABEALPRKTQPGSRRCWFLSFLVAGATFLCLL-----HFGVIGPQREFFKDP 68
Qy 78 EKAPLKGNCSEDLCTLTKSTSKSWAYLOYSKHLNNTKLSW-NEDG---TIHGLIYQD 133
Dy 69 LISPLAQAVRSS-----SRTPSPKPAHV-VANPOAQGLQWLNRNALVANGVELTD 121

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Qy 134 GNLIQFPGLYFIVCOLQFLVQ-CSNHSVDLT---LQLINSKIKKQTLVTV---CE--- 183
Dy 122 NQLVPSGGLYLIYSQVLFGQGCPSNHLVHTHTISIAVSYQTKVNLLSAISKPCQRET 181
Qy 184 -SGVQSKNIYQNLQSOFLHLHYLVQVNSTISVRVDFQYVD 220
Dy 182 PEGAEAPWYEPYVLGGVQLEKGRLSAEINLPDYLD 219

RESULT 14
TNFA_PAPHU STANDARD; PRT; 233 AA.
ID TNFA_PAPHU STANDARD; PRT; 233 AA.
AC O77510;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
TNF OR TNFA.
OS Papio hamadryas ursinus (Chacma baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Papio.
OX NCBI_TaxID=36229;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98147379; PubMed=9488055;
RA Haudek S.B., Redl H., Schlag G., Giroir B.P.;
RT "Complementary DNA (cDNA) sequence of baboon tumor necrosis factor
RT alpha.";
RL Mol. Immunol. 34:1041-1042(1997).
CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA. IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -!- SUBUNIT: HOMOTRIMER.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM.
CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING.
CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF019963; AAC31675.1; -
CC InterPro: IPR000478; -
CC InterPro: IPR002959; -
CC Pfam: PF00229; TNF; 1.
CC PRINTS: PR01234; TNCRSISFCT.
CC PROSITE: PS00251; TNF_1; 1.
CC PROSITE: PS00049; TNF_2; 1.
CC Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
FT PROPEP 1 76 BY SIMILARITY.
FT CHAIN 77 233 TUMOR NECROSIS FACTOR.
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DISULFID 145 177 BY SIMILARITY.
SQ SEQUENCE 233 AA; 25658 MW; B9403255058D4A03 CRC64;

Query Match 6.6%; Score 82.5; DB 1; Length 233;
Best Local Similarity 22.9%; Pred. No. 1.7;

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Matches 50; Conservative 40; Mismatches 101; Indels 27; Gaps 10;

QY 19 AMQVQGVASVWSTPRWSTSRYSFYLS-TTALVCLVAVAIILVVQKKDSTPNTT 77  
Db 13 ABEALPRKTAGQSGRRWFLSFLVAGATTLFCLL---HFGVIGPQREFFPKDPS 68  
QY 78 EKAPLKGNCSDELCTLKSTPSKSKSWAYLQVSKHLNNTKLSW-NEDGT---IHGLIYQD 133  
Db 69 LISPLAQAVRSS-----SRTPSDKPVVHV-VANPQAEGLQWLNRANALLANGVELTD 121  
QY 134 GNLIYVFFGLFIVICOLQFLVO-CSNHSVDLT---LQLLINSKIKKQTLVTV---CE--- 183  
Db 122 NOLVWPSGLIYISQVLFKGGCCSNHLLHTTISRIVAVQTKVNLLSAISKPCQRET 181  
QY 184 -SGVQSKNIYQNLQFLHLYQVNSTISVRVDNFQYVD 220  
Db 182 PEGAEAKWPYEPILYGGVFOLEKGRDLSAEINLPDYLD 219

RESULT 15  
AMPN\_MOUSE  
ID AMPN\_MOUSE STANDARD; PRT; 965 AA.  
AC P97449;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 01-NOV-1997 (Rel. 35, Last annotation update)  
DE AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (CD13)  
DE (P161 MEMBRANE PROTEIN).  
GN ANPEP OR LAP1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=96399091; PubMed=8805562;  
RX Chen H., Kinzer C.A., Paul W.B.;  
RT "p161, a murine membrane protein expressed on mast cells and some  
macrophages, is mouse CD13/aminopeptidase N";  
RL J. Immunol. 157:2593-2600(1996).  
CC -!- CATALYTIC ACTIVITY: AMINOACYL-PEPTIDE + H(2)O = AMINO ACID +  
OLIGOPEPTIDE.  
CC -!- COFACTOR: BINDS ONE ZINC ION.  
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.  
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M1 (ZINC METALLOPROTEASES);  
CC ALSO KNOWN AS THE PEPN SUBFAMILY.  
CC  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
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CC use by non-profit institutions as long as its content is in no way  
CC modified and this statement is not removed. Usage by and for commercial  
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; U77083; AAB19065.1; --  
DR MEROPS: M01.001; --  
DR MGD; MGI:96749; Lapi.  
DR InterPro; IPR000130; --  
DR InterPro; IPR001930; --  
DR Pfam; PF01433; Peptidase\_M1; 1.  
DR PRINTS; PR00756; ALADIPTASE.  
DR PROSITE; PS00142; ZINC\_PROTEASE; 1.  
KW Hydrolase; Metalloprotease; Aminopeptidase; Zinc; Glycoprotein;  
KW Sulfatation; Transmembrane; Duplication; Signal-anchor.  
FT INIT\_MET 0 0  
FT INIT\_MET 0 0  
FT DOMAIN 1 7  
FT TRANSMEM 8 31  
FT DOMAIN 32 67  
FT DOMAIN 68 965  
FT METAL 386 386  
FT ACT\_SITE 387 387  
FT METAL 390 390

FT METAL 409 409 ZINC (CATALYTIC) (BY SIMILARITY).  
FT ACT\_SITE 475 475 PROTON DONOR (POTENTIAL).  
FT REPEAT 68 478  
FT REPEAT 479 898  
FT MOD\_RES 175 175  
FT CARBOHYD 105 105 SULFATATION (POTENTIAL).  
FT CARBOHYD 113 113 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 127 127 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 233 233 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 287 287 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 317 317 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 331 331 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 572 572 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 605 605 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 623 623 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 733 733 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 783 783 N-LINKED (GLCNAC...) (POTENTIAL).  
FT CARBOHYD 816 816 N-LINKED (GLCNAC...) (POTENTIAL).  
SQ SEQUENCE 965 AA; 109503 MW; E450ED27AE94CAA9 CRC64;

Query Match 6.6%; Score 82.5; DB 1; Length 965;  
Best Local Similarity 20.9%; Pred. No. 10;  
Matches 41; Conservative 26; Mismatches 60; Indels 69; Gaps 8;

QY 45 FYLSTT-----ALVCLVAVAIILVVQKKDSTPNTTEKAPLKGNCSDELFT 94  
Db 4 FYISKTGLGILLGVAACVCTIIALSIV---YAEKKNRAENSATAPTLPGSTATTATT 60  
QY 95 LKSTPSKSKWAYLQVSKHL-----NNTKLSWNEDGTHGLIYQDGNLIQV 139  
Db 61 TPAVDESKPNQYRLPKTLIPDAYRVILRPLTPNN-----QGLYIFQGNSTVR 109  
QY 140 FPGLYFIVCQLFVQCSN-----HSVDLTQLLLINSKIKKOTLVTVCSGVQSKNIY 192  
Db 110 F-----TCNQTDVIIHSKKNLTGKGNHRVVLRTL-----DGTTPAPNID 150  
QY 193 Q-----NLSQFLHLYLQ 204  
Db 151 KTELVERTEYLVVHLQ 166

Search completed: September 5, 2001, 10:29:51  
Job time: 396 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2001, 10:21:50 ; Search time 31.97 Seconds  
(without alignments)  
569.463 Million cell updates/sec

Title: US-09-628-126-6  
Perfect score: 1246  
Sequence: 1 MEPLQAGSCGAPSPDPAM.....DTNTPLDNLSVFLYSSD 239  
Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1246	100.0	239	2 B40710	CD30 ligand - mous
2	860.5	69.1	234	2 A40710	CD30 ligand - huma
3	123	9.9	279	2 A53062	Fas ligand - mouse
4	102	8.2	278	2 A43266	fas ligand - rat
5	91	7.3	309	2 I53384	4-lBB ligand - mou
6	89.5	7.2	235	2 I54490	tumor necrosis fac
7	89.5	7.2	401	2 S74767	hypothetical prote
8	87	7.0	281	2 I38707	Fas ligand - human
9	87	7.0	2013	2 C71610	probable membrane
10	86.5	6.9	2195	2 S61103	SEC16 protein - ye
11	86	6.9	674	2 S61181	hypothetical prote
12	85.5	6.9	994	2 H96510	probable disease r
13	84.5	6.8	884	2 T02731	serine/threonine-s
14	84	6.7	1110	2 F84547	probable disease r
15	83	6.7	889	2 T45691	receptor-like prot
16	82	6.6	234	1 JH0529	tumor necrosis fac
17	82	6.6	665	2 T05082	protein kinase hom
18	81.5	6.5	304	2 T27593	hypothetical prote
19	81.5	6.5	304	2 T27594	hypothetical prote
20	81	6.5	866	2 T10587	serine/threonine-s
21	81	6.5	890	2 C96654	hypothetical prote
22	80.5	6.5	344	2 T05104	hypothetical prote
23	80.5	6.5	663	2 H96533	hypothetical prote
24	80	6.4	165	2 H64460	hypothetical prote
25	80	6.4	369	2 S77028	protein kinase, 41
26	79.5	6.4	383	2 S67813	probable membrane
27	79.5	6.4	818	2 T02823	cell surface prote
28	79.5	6.4	1402	2 T17456	NUD1 protein - yea
29	79	6.3	851	2 S67285	

30 78.5 6.3 234 1 J01344 tumor necrosis fac  
31 78.5 6.3 235 2 J00029 tumor necrosis fac  
32 78.5 6.3 960 2 T24221 hypothetical prote  
33 78.5 6.3 1150 2 S49956 probable membrane  
34 78.5 6.3 1706 2 I84499 zinc finger protei  
35 78 6.3 396 1 BMH02 bone morphogenetic  
36 78 6.3 427 2 T40064 hypothetical prote  
37 78 6.3 616 2 T32131 hypothetical prote  
38 78 6.3 859 1 VCLJMN env polypeptide pr  
39 77.5 6.2 463 2 S37962 probable purine nu  
40 77.5 6.2 1583 2 S59644 sister chromatid c  
41 77 6.2 428 2 T48284 hypothetical prote  
42 77 6.2 568 2 T20421 hypothetical prote  
43 77 6.2 686 2 F96542 probable protein k  
44 77 6.2 769 2 T39089 hypothetical prote  
45 77 6.2 795 2 H84944 phenylalanine--trn

ALIGNMENTS

RESULT 1  
B40710  
CD30 ligand - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 05-Nov-1999  
C:Accession: B40710  
R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, Alderson, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, Cell 73, 1349-1360, 1993  
A:Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de  
A:Reference number: A40710; MUID:93313964  
A:Accession: B40710  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-239 <SMI>  
A:Cross-references: GB:L09754; NID:g349288; PIDN:AAA74595.1; PID:g349289  
C:Keywords: cytokine receptor; membrane protein; surface antigen

Query Match 100.0%; Score 1246; DB 2; Length 239;  
Best Local Similarity 100.0%; Pred. No. 6.4e-106; Indels 0; Gaps 0;  
Matches 239; Conservative 0; Mismatches 0;

QY 1 MEPLQAGSCGAPSPDPAMQVPGSVASVAPWRSRSTPRWSTSRSYFLSTALVCLVAVA 60  
DB 1 MEPLQAGSCGAPSPDPAMQVPGSVASVAPWRSRSTPRWSTSRSYFLSTALVCLVAVA 60  
QY 61 IILVLVQKDSPTNTTEKAPLKGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSW 120  
DB 61 IILVLVQKDSPTNTTEKAPLKGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSW 120  
QY 121 NEDGTIHLIYODGNLIYVFCGLYFVCOLOFLVOCNHSVDLTQLLINSKIKQTIVT 180  
DB 121 NEDGTIHLIYODGNLIYVFCGLYFVCOLOFLVOCNHSVDLTQLLINSKIKQTIVT 180  
QY 181 VCESGVQSKNIYQNLSQLLLHYLVQNSVTISVRVDNFQVDTNTFFLDNVLSVFLYSSSD 239  
DB 181 VCESGVQSKNIYQNLSQLLLHYLVQNSVTISVRVDNFQVDTNTFFLDNVLSVFLYSSSD 239

RESULT 2  
A40710  
CD30 ligand - human  
C:Species: Homo sapiens (man)  
C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 21-Jul-2000  
C:Accession: A40710  
R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, Alderson, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, Cell 73, 1349-1360, 1993  
A:Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de  
A:Reference number: A40710; MUID:93313964  
A:Accession: A40710

2

	Qy	18	PAMQVPGSVASPWSTRPWRSTSRSYFYLSITTAIVCLVVAVAILLVLVQKDSPTNT	77
			:   :	
	Db	59	PAYNVADREAA--WPPALNFCSRHPKLGLYVALVLLIIILIIAACVPIFTETPRPALTTTS	116
			:   :	
	Qy	78	EKAPLKGGNCSE-----DLFCTLKSTPSKKSWAYLQVSKH--LNNTKLSM-NEDGT----	125
			:   :   :	
	Db	117	PNLGTRNNADQVTVPVSHIGCPNWTQQGSPVFAKLLAKNOASCNTTLNHSQDGAGSSY	176
			:   :   :	
	Qy	126	-IHGLIYODG--NLVIQFPGLYIVCQLQFLVOCSN--HSVDTLTQLLINSIKKOTL--	178
			:   :     :   :	
	Db	177	LSOGLRAYEEDKELVSDSPGLYVVELLELSPFTTWTGHKVGSWSVLVLQAQPQVDDEFD	236
			:   :   :	
	Qy	179	----VTVCSGVOSKNIIQNLSOFLL-----HYLQV-----NSTISVRVDNFQYYDDTNT	223
			:   :   :   :	
	Db	237	LALTVELFPCSMENKLVDRSWSQALLLKAGRHLRSLVGRLAYLHGCAQDAYRDWELLYPNTTS	296
			:   :   :	





Db 102 FOLFHLQKELARESTSQMHTASSLEKQIGHPS-----PPPEKKELRKVAHITGKS 153  
Qy 112 HLNNTKLSWNEGTI---HGLIYQDGNLIVQPPGLYFIVCQLQFLVQ-CSN-----HSVDL 163  
Db 154 NSRSPLEWEDYIGVLLSGVYKKGGLVNETGLYFVYSKYVFGQSCNNLPSHKV-- 211  
Qy 164 TLQLLINSK-----IKQTLVTVCEG-----VQSKNYIYQNLSQFLHHY 202  
Db 212 ---YMRNSKYPQDLVMMECKMMSYCTTGOMWARSSYLGAVENTLSADHLVYVNVSELSLVN 268  
Qy 203 LQVNST 208  
Db 269 FEESQT 274  
RESULT 9  
C71610  
probable membrane associated protein PFB0615c - malaria parasite (Plasmodium falciparum)  
C:Species: Plasmodium falciparum  
C:Date: 13-Nov-1998 #sequence\_revision 13-Nov-1998 #text\_change 21-Jul-2000  
R:Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;  
; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.  
Science 282, 1126-1132, 1998  
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.  
A:Reference number: A71600; MUID:99021743  
A:Accession: C71610  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-2013 <GAR>  
A:Cross-references: GB:AF001406; GB:AE001362; NID:g3845230; PIDN:AAC71912.1; PID:g384523  
A:Experimental source: clone 3D7  
C:Genetics:  
A:Gene: PFB0615c  
Query Match 7.0%; Score 87; DB 2; Length 2013;  
Best Local Similarity 23.9%; Pred. No. 22;  
Matches 34; Conservative 31; Mismatches 49; Indels 28; Gaps 7;  
Qy 88 SEDLFTLKSTPSKSWAYLQVSKHLNWKLSWNEGTTHGLIYQDGNLIVQPPGLYFIV 147  
Db 16 SDNIFCFLKD-----GYICFMNLLN-----NEKKYLYIFCSQDEGYVAQY---YFDV 59  
Qy 148 COLOFLVQCSNHSVDLTQLQLT-----NSKIKKOTLVTVCEGVSQSKNIYQNLSQFLH--- 200  
Db 60 VKCRYEKKEEDCNKMTINIMLLQNNKKIKETCYI---KNVVTNKIYHTL--FLVINK 114  
Qy 201 HYLQVNSTISVRVDNFOYVDN 222  
Db 115 HYHNILCSLSPENNSFEILTNN 136  
RESULT 10  
S61103  
SEC16 protein - yeast (Saccharomyces cerevisiae)  
N:Alternate names: protein Lpf1w; protein YPL085w  
C:Species: Saccharomyces cerevisiae  
C:Date: 23-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 06-Feb-1998  
R:Hall, J.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.; Vo, D.H.; Wa  
submitted to the EMBL Data Library, August 1995  
A:Description: The sequence of Saccharomyces cerevisiae  
A:Reference number: S59677  
A:Accession: S61103  
A:Molecule type: DNA  
A:Residues: 1-2195 <HAL>  
A:Cross-references: EMBL:U41849; NID:g1147608; PID:g1147609; MIPS:YPL085w  
C:Genetics:  
A:Gene: SGD:SEC16  
A:Cross-references: SGD:S0006006; MIPS:YPL085w  
A:Map position: 16L  
C:Keywords: transmembrane protein

F:1198-1214/Domain: transmembrane #status predicted <TM1>  
F:1250-1266/Domain: transmembrane #status predicted <TM2>  
Query Match 6.9%; Score 86.5; DB 2; Length 2195;  
Best Local Similarity 20.9%; Pred. No. 27;  
Matches 53; Conservative 39; Mismatches 87; Indels 75; Gaps 13;  
Qy 26 SVASPWRSTRP-----WRSTSRSYF-----YLTSTALVCLVVA 58  
Db 970 SVAPPQRENPIKIDNEALLRRQPIFHWSAANKVYAVPIPPQSQYMISSIVQEIKV 1029  
Qy 59 VAILVLVQKKD---STPNTEKAPLKGGNCSEDLCTLKSTPSKKS-----WAYLQV 109  
Db 1030 TPI--DQIIKPNMDLKSFPGPLGSAKLKKKDLTKWMTTIKISINESSTDTMTIWLLE 1087  
Qy 110 SKHLNWKLSWNEGTTHGLIYQDGNLIV-----QPPGLY--FIVCQLQFL--VQ 155  
Db 1088 KL---NDKVNWK---NISKLLYNSDELLMYLSQPPFGDMIPNAYRLDINQMRVLAFLQ 1141  
Qy 156 CSNHSV-----DLTLQLLINSKIKKOTLVTVCEGVSQSKNIYQNLSQFLH 201  
Db 1142 TGNHDEALRLALSARDYAIALLVGLSGMKDRWSEVIQKLYEGTAGPNQOKELAHFLLL 1201  
Qy 202 YLQV---NSTISVR 212  
Db 1202 IFQVFGNSKMAIK 1215  
RESULT 11  
S61181  
hypothetical protein YDR295c - yeast (Saccharomyces cerevisiae)  
N:Alternate names: hypothetical protein D9740.10  
C:Species: Saccharomyces cerevisiae  
C:Date: 23-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 23-Mar-2001  
C:Accession: S61181  
R:Ding, H.  
submitted to the EMBL Data Library, June 1995  
A:Description: The sequence of S. cerevisiae cosmid 9740.  
A:Reference number: S61160  
A:Accession: S61181  
A:Molecule type: DNA  
A:Residues: 1-674 <DIN>  
A:Cross-references: EMBL:U28374; NID:g849207; PID:g849217; GSPDB:GN00004; MIPS:YDR295  
C:Genetics:  
A:Gene: MIPS:YDR295c  
A:Map position: 4R  
Query Match 6.9%; Score 86; DB 2; Length 674;  
Best Local Similarity 25.0%; Pred. No. 7.1;  
Matches 40; Conservative 30; Mismatches 60; Indels 30; Gaps 9;  
Qy 70 KDSTPNTEKAPLKGGNCSEDLCTLKSTPSK-----SWAYLQVSKHLNNTK- 117  
Db 192 KDGTPNSVSTSSNSNSTSYTGYSKDDYDYSVRNLKRRKINTDDMLFLATTKLKHQDY 251  
Qy 118 LSWNEGTTHGLIYQDGNLIVQPPGLYFI-----VCLOFLVQCSNHSVDLTQLLIN 170  
Db 252 LLANYD--IDMIISFDPMLEVPALQVLRNNAKNDPIIKLLVQ-----HYLLD 303  
Qy 171 SKIKKOTLVTV--VCEG-VQSKNIYQNLSQFLHLYQVNS 207  
Db 304 SEIKNSVSKSHLSNNGHVDDSQFYEIKSSLLYFLQARN 343  
RESULT 12  
H96510  
probable disease resistance protein [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: H96510  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719  
A:Accession: H96510  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-994 <STO>  
A:Cross-references: GB:AE005173; NID:g11321768; PIDN:AAG34245.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: F2G19.6  
A:Map position: 1

Query Match 6.9%; Score 85.5; DB 2; Length 994;  
Best Local Similarity 26.3%; Pred. No. 13;  
Matches 40; Conservative 21; Mismatches 64; Indels 27; Gaps 8;  
QY 107 LOVSKHLNNTKLSWE-DGTIHLI-----YQDGNLIVQFGLYFIVCOLOFLVQ 155  
Db 322 LRLSLHLNVLSENNFVGEIPSSVNLKQLTLDVSDNNLNGFSSLLNLNQLRVIDI 381  
QY 156 CSNHSVDLTQLLINSKIRKQTIVTVCSGVQSK-----NIYQNLSQFLHLVQVNSTI 209  
Db 382 CSNHFTGLPPRI--SOLSNLEFESACDSFTGISLFLNI--SSLTGLSYNLNDTT 438  
QY 210 SVR----VDNFQ--YVDNTTFPLDNY-LSVFL 234  
Db 439 NIKNLSLHLNQLRLDNNFRASQVDLDVFL 470

RESULT 13  
T02731  
serine/threonine-specific protein kinase (EC 2.7.1.1) T9I4.7 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 16-Feb-2001  
C:Accession: T02731; D84691  
R:Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, M.; Ron  
submitted to the EMBL Data Library, August 1998  
A:Description: Arabidopsis thaliana chromosome II BAC T9I4 genomic sequence.  
A:Reference number: Z14710  
A:Accession: T02731  
A:Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-884 <ROU>  
A:Cross-references: EMBL:AC005315; NID:g3461834; PIDN:AAC33227.1; PID:g3461841; GSPDB:GN  
A:Experimental source: cultivar Columbia  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487  
A:Accession: D84691  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-884 <STO>  
A:Cross-references: GB:AE002093; NID:g3461841; PIDN:AAC33227.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: ATSP:T9I4.7; At2g28990  
A:Map position: 2  
A:Introns: 24/1; 203/2; 362/1; 410/2; 434/2; 458/2; 484/2; 538/1; 621/3; 664/1; 686/1; 7  
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homol  
C:Keywords: phosphotransferase; protein kinase

Query Match 6.8%; Score 84.5; DB 2; Length 884;

Best Local Similarity 25.1%; Pred. No. 14;  
Matches 52; Conservative 28; Mismatches 76; Indels 51; Gaps 12;  
QY 48 STTALVCLVAVAILLVVQVKDSTPNTTEKAPL-----KGGNC-SDLEFCTTKSPSK 101  
Db 512 SAASLVIVVVVA--LFFVFRKKASPSNLHAPPSPVSNPGHNSQSESSF-----TSKK 564  
QY 102 KSWAYLOVSKHLNNTKLSWNEGDG---TIHGLIYQDGNLIVQFGLYFIVCOLOFLVQCSN 158  
Db 565 IRFTYSEVQEQNTNFDKALGEGGVVYHGFV---NVIEQ-----VAVKLLSQSSS 612  
QY 159 H-----SVDLTQLLINSKIRKQTIVTVCSGVQSKNIYQ-----NLSOFL-----H 201  
Db 613 QGYKHFAEVELLMRV---HHNLVSLVGYCDEGEHLAIYEYMPNGDLKQHLKSKHGGF 669  
QY 202 YLQVNSTISVRVD---NFQYVDVTNTP 225  
Db 670 VLSWESRLKIVLDAALGLEYLHTGCV 696

RESULT 14  
F84547  
probable disease resistance protein [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C:Accession: F84547  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487  
A:Accession: F84547  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1110 <STO>  
A:Cross-references: GB:AE002093; NID:g6598362; PIDN:AAF18600.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g17060  
A:Map position: 2

Query Match 6.7%; Score 84; DB 2; Length 1110;  
Best Local Similarity 22.7%; Pred. No. 20;  
Matches 44; Conservative 36; Mismatches 66; Indels 48; Gaps 10;  
QY 46 YLSTALVCLVAV---AIIIV-----LVVQKDSPTNTEKAPLKGKNCSEDLFCTL 95  
Db 680 YLQGTAKRCPTSTENLQKLLDLKCEVLSPLDCGLGNLRSLOELILSGCSK-----L 734  
QY 96 KSTPSKRSWAYLOVSKHLNNTKLSWNEGDGTHGLIYQDGNLIVQFGLYFIVCOLOFLVQ 155  
Db 735 KFFPELK-----ETMKSIK-----ILLDGTAKOMPIL--LQC-----IQ 768  
QY 156 CSNHSV-DLTQLLINSKIRKQTIVTVCSGVQSKNIYQNLSQ-FLHLYQVNS-----T 208  
Db 769 SQGHSVANKTLPNSLDYLPSSLLSLCLSGNDIESLHANISQLYHLKWLDKNCKKLKS 828  
QY 209 ISVRVDNFQYVDN 222  
Db 829 VSVLPPLNKLCLDAH 842

RESULT 15  
T45691  
receptor-like protein kinase homolog - Arabidopsis thaliana  
N:Alternate names: protein F18L15.60  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Mar-2000  
C:Accession: T45691  
R:Choisne, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.;  
submitted to the Protein Sequence Database, November 1999  
A:Reference number: Z23010

A: Accession: T45691  
 A: Status: preliminary  
 A: Molecule type: DNA  
 A: Residues: 1-889 <CHO>  
 A: Cross-references: EMBL:AL133298  
 A: Experimental source: cultivar Columbia; BAC clone F18L15  
 C: Genetics:  
   A: Map position: 3  
   A: Introns: 31/1; 211/2; 370/1; 418/2; 442/2; 466/2; 546/1; 630/3; 673/1; 695/1; 7  
   A: Note: F18L15\_60  
 C: Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

Search completed: September 5, 2001, 10:23:51  
Job time: 121 sec

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	181.5	14.6	95	5	US-09-758-468-439	Sequence 439, Appl
2	119	9.6	55	1	PCT-US01-08656-9656	Sequence 9656, Ap
3	102	8.2	278	1	PCT-US01-21282-6	Sequence 6, Appl
4	102	8.2	278	5	US-09-899-059-6	Sequence 6, Appl
5	83.5	6.7	362	5	US-09-764-853-532	Sequence 532, App
6	83.5	6.7	523	1	PCT-US01-10472-300	Sequence 300, App
7	80.5	6.5	233	1	PCT-US01-21282-3	Sequence 3, Appl
8	80.5	6.5	233	5	US-09-879-919-5	Sequence 5, Appl
9	80.5	6.5	233	5	US-09-899-059-3	Sequence 3, Appl
10	79	6.3	350	1	PCT-US01-16450-2513	Sequence 2513, Ap
11	79	6.3	360	5	US-09-758-472-8446	Sequence 8446, Ap
12	78.5	6.3	271	1	PCT-US01-16450-2658	Sequence 2658, Ap
13	78	6.3	341	1	PCT-US01-14827-10562	Sequence 10562, A
14	78	6.3	397	5	US-09-813-398-24	Sequence 24, Appl
15	78	6.3	426	5	US-09-868-604-8	Sequence 8, Appl
16	76.5	6.1	251	1	PCT-US01-21282-20	Sequence 20, Appl
17	76.5	6.1	251	5	US-09-899-059-20	Sequence 20, Appl
18	76.5	6.1	317	5	US-09-577-780-13	Sequence 13, Appl
19	76	6.1	2367	1	PCT-US01-14827-9813	Sequence 9813, Ap
20	75	6.0	424	1	PCT-US01-16450-2690	Sequence 2690, Ap
21	75	6.0	1014	1	PCT-US01-14827-14206	Sequence 14206, A
22	74.5	6.0	198	5	US-09-738-626-4749	Sequence 4749, Ap
23	74.5	6.0	238	5	US-09-839-894-2	Sequence 2, Appl
24	74.5	6.0	1103	5	US-09-570-581A-1840	Sequence 1840, Ap
25	74.5	6.0	1103	5	US-09-573-655A-338	Sequence 338, App
26	74.5	6.0	1103	5	US-09-573-655A-656	Sequence 656, Ap
27	73.5	5.9	309	1	PCT-US01-10739-8	Sequence 8, Appl





Query Match	6.5%	Score 80.5;	DB 5;	Length 233;
Best Local Similarity	24.3%	Pred. No. 3.5;		
Matches 49:	Conservative	37: Mismatches	85: Indels	31: Gaps
10:				

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41 SRSIFLSTIALVCLLVAAILD-----VLVWUKKUSIPMITKAPLKGNGCSEDLFC 93
b 27 SRRCLFLSLFSF--LIVAGATTFLCLLHFGVIGPQREESPRDLISLISPLAQAVRSS---80
y 94 TLKSTPSKSWAYLOVSKSHLNTKLSW--NEDGT---IHGLIYODGNLIIVQFPGLYFIVCQ 149
b 81 --SRTPSDKPAHV--VANPQAEQQLWLNRRRANALLANGVELRDNLQVLVVPSEGLIYISQ 137
y 150 IAFVLO--CSNHSVDLT---LQLLINSKTKKQTLVTV---CE-----SGVOSKNIYNLQSOF 198
b 138 VLFGKGCGCPSTHLLTHTTISRTIAVSQYTKVNLLSAIKPCQRETPEGAEAKPWYEVILG 197
y 199 LLHYLQVNSTISVRVDNFQYVD 220
b 198 GVQLEKGDRLSAEINRPDYLD 219

RESULT 10
BT-US01-16450-2513
Sequence 2513, Application PC/TUS0116450

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APPLICANT: Human Genome Sciences, Inc.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA131PCT
CURRENT APPLICATION NUMBER: PCT/US01/16450
CURRENT FILING DATE: 2001-06-01
PRIOR APPLICATION NUMBER: 60/205,515
PRIOR FILING DATE: 2000-05-19
NUMBER OF SEQ ID NOS: 2820
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2513
LENGTH: 350
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (13)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (45)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (123)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
CT-US01-16450-2513

Query Match          6.3%; Score 79; DB 1; Length 350;
Best Local Similarity 25.3%; Pred. No. 8.4;
Matches 40; Conservative 25; Mismatches 55; Indels 38; Gaps 7;

1 51 ALVCLVAVAI-----ILVLVOKDS-----TPNTTEKAPLKGNCSED 90
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
167 AILHLVSLAMHFRAPIRLPETHVTQVVVVRKREGLLHSSHISELTITTEMGMGRFERD 226
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

1 91 LECTL-----KSTSEKSKWAYLQVSKHLNNTKLSWNEDGTHGLHYODGNLIYQFPGL- 143
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
227 AFDTTLDHAPDGLSVVVRKSLITF-VNKHNLKLNLEVTLET----QFADGVYVLLMGLL 281
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

1 144 --YFTVCQLQFLVQCS---NHSVDLTLLQLINSKIKK 175
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
282 EDYFVPLHHFYLTPTSEFDQKVHNVSFAPFLMDGLKK 319
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 11
3-09-758-472-8446
Sequence 8446. Application US/09758472

```

## RESULT 11

RESOLV II  
US-09-758-472-8446

US-09-738-472-8440  
: Sequence 8446. Application US/09758472

; sequence 8446, Application 03/03/38472  
: GENERAL INFORMATION:

Query Match	6.3%	Score 78.5;	DB 1;	Length 271;
Best Local Similarity	22.1%;	Pred. No. 6.7;		
Matches	40;	Conservative 36;	Mismatches 74;	Indels 31; Gaps 6;
Qy	35	RPNWSTRSYFYLSTTALVCLWAV-AIILVLVQVKDSTPTTEKAPLKGNGCSEDLFC	93	
	:	: : : : : :	:	:
	:	: : : : : :	:	:
Db	20	QPYLDTLRQEQLQQDPILLSVVAVALLTLVPFKLIIRSSORAVLLVGLCD----	74	
	:	: : : : : :	:	:
Qy	94	TLKSTPSKKSWAYLQVSKHL-NNTKLWNEDGTHGLIYQDGNLTVPFGLYFIYVCLOQF	152	
	:	: : : : : :	:	:
Db	75	-----SGKTLLFYRLTGLYRDQTSTDCSAVVRVNNRGNSLT-----	114	
	:	: : : : : :	:	:
Qy	153	LVOCSNHSDVLTQLLINSKITKOTLVTVCESGV---QSKNIYQNLSQFLHLYQVNSTI	209	
	:	: : : : : :	:	:





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2001, 10:21:45 ; Search time 25.09 Seconds  
(without alignments)  
196.138 Million cell updates/sec

Title: US-09-628-126-6  
Perfect score: 1246  
Sequence: 1 MFGLQAGSCGAPSPDPAM.....DTNTFFLDNLVSLYSSD 239

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1246	100.0	239	1 US-08-225-989-6	Sequence 6, Appli
2	1246	100.0	239	1 US-08-570-923-6	Sequence 6, Appli
3	1246	100.0	239	1 US-08-580-014-6	Sequence 6, Appli
4	1246	100.0	239	4 US-09-079-785-6	Sequence 19, Appli
5	1141	91.6	220	1 US-08-225-989-19	Sequence 19, Appli
6	1141	91.6	220	1 US-08-570-923-19	Sequence 19, Appli
7	1141	91.6	220	1 US-08-580-014-19	Sequence 19, Appli
8	1141	91.6	220	4 US-09-079-785-19	Sequence 19, Appli
9	860.5	69.1	234	1 US-08-225-989-8	Sequence 8, Appli
10	860.5	69.1	234	1 US-08-570-923-8	Sequence 8, Appli
11	860.5	69.1	234	1 US-08-580-014-8	Sequence 8, Appli
12	860.5	69.1	234	4 US-09-079-785-8	Sequence 8, Appli
13	814.5	65.4	215	1 US-08-225-989-23	Sequence 23, Appli
14	814.5	65.4	215	1 US-08-570-923-23	Sequence 23, Appli
15	814.5	65.4	215	1 US-08-580-014-23	Sequence 23, Appli
16	814.5	65.4	215	4 US-09-079-785-23	Sequence 23, Appli
17	685	55.0	130	1 US-08-225-989-21	Sequence 21, Appli
18	685	55.0	130	1 US-08-570-923-21	Sequence 21, Appli
19	685	55.0	130	1 US-08-580-014-21	Sequence 21, Appli
20	685	55.0	130	4 US-09-079-785-21	Sequence 21, Appli
21	624	50.1	148	3 US-08-584-031-12	Sequence 12, Appli
22	391.5	31.4	125	1 US-08-225-989-20	Sequence 20, Appli
23	391.5	31.4	125	1 US-08-570-923-20	Sequence 20, Appli
24	391.5	31.4	125	1 US-08-580-014-20	Sequence 20, Appli
25	391.5	31.4	125	4 US-09-079-785-20	Sequence 20, Appli
26	229	18.4	52	4 US-09-369-494-17	Sequence 17, Appli
27	115	9.2	279	5 PCT-US95-00362-5	Sequence 5, Appli

28 91 7.3 309 1 US-08-236-918A-2 Sequence 2, Appli  
29 87 7.0 281 2 US-08-810-453-2 Sequence 2, Appli  
30 87 7.0 281 3 US-08-815-190A-2 Sequence 2, Appli  
31 87 7.0 281 4 US-09-290-640-25 Sequence 25, Appli  
32 87 7.0 281 4 US-09-479-524-3 Sequence 3, Appli  
33 87 7.0 281 5 PCT-US95-00362-2 Sequence 2, Appli  
34 85 6.8 291 1 US-08-670-354-6 Sequence 6, Appli  
35 85 6.8 291 5 PCT-US96-10895-6 Sequence 6, Appli  
36 83.5 6.7 287 3 US-08-815-190A-16 Sequence 16, Appli  
37 83 6.7 550 2 US-08-417-210A-140 Sequence 140, App  
38 83 6.7 551 2 US-08-417-210A-137 Sequence 137, App  
39 83 6.7 551 2 US-08-417-210A-143 Sequence 143, App  
40 83 6.7 857 1 US-08-022-835-4 Sequence 4, Appli  
41 83 6.7 857 1 US-08-388-809-4 Sequence 4, Appli  
42 83 6.7 857 2 US-08-647-714-4 Sequence 8, Appli  
43 82.5 6.6 183 4 US-09-105-343A-8 Sequence 2, Appli  
44 82 6.6 396 2 US-07-989-847-2 Sequence 2, Appli  
45 82 6.6 396 4 US-08-469-411-2 Sequence 2, Appli

## ALIGNMENTS

RESULT 1  
US-08-225-989-6  
; Sequence 6, Application US/08225989  
; Patent No. 5480981  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-570-923-6

Query Match 100.0%; Score 1246; DB 1; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.2e-116;
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MEPGLQAGSCGAPSPDPAMQVQPGSVASPMRSTRPWRSTSRSYFYLTALVCLVVAVA 60
DB 1 MEPGLQAGSCGAPSPDPAMQVQPGSVASPMRSTRPWRSTSRSYFYLTALVCLVVAVA 60
QY 61 IILVLVQKKDSTNTTEKAPLKGNGCSEDLFCTLKSTPSKSWAYLOVSKHLNNTKLSW 120
DB 61 IILVLVQKKDSTNTTEKAPLKGNGCSEDLFCTLKSTPSKSWAYLOVSKHLNNTKLSW 120
QY 121 NEDGTIIGLIYQDGNLIVQPPGLYFIVCOLQFLVQCSNHSVDLTLQLLINSIKKKQTLVT 180
DB 121 NEDGTIIGLIYQDGNLIVQPPGLYFIVCOLQFLVQCSNHSVDLTLQLLINSIKKKQTLVT 180
QY 181 VCESGVQSKNIYQNLQSOFLHLHYLOVNSTISVRVDNFQYVDNTFPLDNVLSVFLYSSD 239
DB 181 VCESGVQSKNIYQNLQSOFLHLHYLOVNSTISVRVDNFQYVDNTFPLDNVLSVFLYSSD 239

RESULT 3
US-08-580-014-6
; Sequence 6, Application US/08580014
; Patent No. 5753203
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,014
; FILING DATE: 20-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992

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CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-580-014-6

Query Match 100.0%; Score 1246; DB 1; Length 239;  
Best Local Similarity 100.0%; Pred. No. 1.2e-116;  
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MEPGLQAGSCGAPSPDPAMQVPGSVASVWSTRTSPWSTSRYSYFYLSTTALVCLVAVA 60  
Db 1 MEPGLQAGSCGAPSPDPAMQVPGSVASVWSTRTSPWSTSRYSYFYLSTTALVCLVAVA 60  
Qy 61 IILVLVQKKDSTPNTTEKAPLKGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSW 120  
Db 61 IILVLVQKKDSTPNTTEKAPLKGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSW 120  
Qy 121 NEDGTIHLIYQDGNLIVQFPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVT 180  
Db 121 NEDGTIHLIYQDGNLIVQFPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVT 180  
Qy 181 VCESGVQSKNIYQNLISQFLHLYQVNSTISVRVDNFQYVDNTFPDLNVLVSFLYSSSD 239  
Db 181 VCESGVQSKNIYQNLISQFLHLYQVNSTISVRVDNFQYVDNTFPDLNVLVSFLYSSSD 239

RESULT 4  
US-09-079-785-6  
Sequence 6, Application US/09079785  
Patent No. 6143869  
GENERAL INFORMATION:  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
APPLICANT: Armitage, Richard J.  
APPLICANT: Gruss, Hans-Jurgen  
TITLE OF INVENTION: No. 6143869el Cytokine That Binds CD30  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1

SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,785  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,989  
FILING DATE: 12 APRIL 1994  
APPLICATION NUMBER: US 07/966,775  
FILING DATE: 27-OCT-1992  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 239 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-079-785-6

Query Match 100.0%; Score 1246; DB 4; Length 239;  
Best Local Similarity 100.0%; Pred. No. 1.2e-116;  
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MEPGLQAGSCGAPSPDPAMQVPGSVASVWSTRTSPWSTSRYSYFYLSTTALVCLVAVA 60  
Db 1 MEPGLQAGSCGAPSPDPAMQVPGSVASVWSTRTSPWSTSRYSYFYLSTTALVCLVAVA 60  
Qy 61 IILVLVQKKDSTPNTTEKAPLKGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSW 120  
Db 61 IILVLVQKKDSTPNTTEKAPLKGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSW 120  
Qy 121 NEDGTIHLIYQDGNLIVQFPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVT 180  
Db 121 NEDGTIHLIYQDGNLIVQFPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVT 180  
Qy 181 VCESGVQSKNIYQNLISQFLHLYQVNSTISVRVDNFQYVDNTFPDLNVLVSFLYSSSD 239  
Db 181 VCESGVQSKNIYQNLISQFLHLYQVNSTISVRVDNFQYVDNTFPDLNVLVSFLYSSSD 239

RESULT 5  
US-08-225-989-19  
Sequence 19, Application US/08225989  
Patent No. 5480981  
GENERAL INFORMATION:  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
APPLICANT: Armitage, Richard J.  
APPLICANT: Gruss, Hans-Jurgen  
TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,989  
FILING DATE: 12 APRIL 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/966,775  
FILING DATE: 27-OCT-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 220 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-225-989-19

Query Match 91.6%; Score 1141; DB 1; Length 220;  
Best Local Similarity 100.0%; Pred. No. 3.2e-106;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 MOVQPGSVASPRWSTSRSFYLSLTALVCLVAVAILLVVQKDKSTPNTTEK 79  
Db 1 MOVQPGSVASPRWSTSRSFYLSLTALVCLVAVAILLVVQKDKSTPNTTEK 60  
QY 80 APLKGGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQV 139  
Db 61 APLKGGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQV 120  
QY 140 FPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQFLVTVCGSGVSKNIYQNLSQL 199  
Db 121 FPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQFLVTVCGSGVSKNIYQNLSQL 180  
QY 200 LHYLVNSTLSVRVDNQYVDNTFFPLDNLVLSVLYSSD 239  
Db 181 LHYLVNSTLSVRVDNQYVDNTFFPLDNLVLSVLYSSD 220

## RESULT 6

US-08-570-923-19

; Sequence 19, Application US/08570923

; Patent No. 5677430

GENERAL INFORMATION:  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
APPLICANT: Armitage, Richard J.  
APPLICANT: Gruss, Hans-Jurgen  
TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/570,923  
FILING DATE: 12-DEC-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,989  
FILING DATE: 12 APRIL 1994  
APPLICATION NUMBER: US 07/966,775  
FILING DATE: 27-OCT-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 220 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-570-923-19

Query Match 91.6%; Score 1141; DB 1; Length 220;  
Best Local Similarity 100.0%; Pred. No. 3.2e-106;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 MOVQPGSVASPRWSTSRSFYLSLTALVCLVAVAILLVVQKDKSTPNTTEK 79  
Db 1 MOVQPGSVASPRWSTSRSFYLSLTALVCLVAVAILLVVQKDKSTPNTTEK 60  
QY 80 APLKGGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQV 139  
Db 61 APLKGGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQV 120  
QY 140 FPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQFLVTVCGSGVSKNIYQNLSQL 199  
Db 121 FPGLYFIVCQLQFLVQCSNHSVDLTQLLLINSKIKKQFLVTVCGSGVSKNIYQNLSQL 180

QY 200 LHYLOVNSTISVRVDFQYVDTNTFPDLNVLVSFLYSSD 239  
Db 181 LHYLOVNSTISVRVDFQYVDTNTFPDLNVLVSFLYSSD 220

## RESULT 7

US-08-580-014-19  
; Sequence 19, Application US/08580014  
; Patent No. 5753203  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/580,014  
; FILING DATE: 20-DEC-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 220 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-580-014-19

Query Match 91.6%; Score 1141; DB 1; Length 220;  
Best Local Similarity 100.0%; Pred. No. 3.2e-106;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 MQVQPGSVASPRSTRPWRSTSRSYFLSTALVCLVAVAILLVVQKKDSTPNTTEK 79

Db 1 MQVQPGSVASPRSTRPWRSTSRSYFLSTALVCLVAVAILLVVQKKDSTPNTTEK 60  
QY 80 APLKGGNCSEDLCTLKSTPSKKSWAYLQVSKHLNNTKLSWNEDGTIHLGIYQDGNLIYQ 139  
Db 61 APLKGGNCSEDLCTLKSTPSKKSWAYLQVSKHLNNTKLSWNEDGTIHLGIYQDGNLIYQ 120  
QY 140 FPGLYFIVCQLQFLVQCSNHSVDLTLQLLINSKIKKQTLVTVCESGVQSKNIYONLSQFL 199  
Db 121 FPGLYFIVCQLQFLVQCSNHSVDLTLQLLINSKIKKQTLVTVCESGVQSKNIYONLSQFL 180  
QY 200 LHYLOVNSTISVRVDFQYVDTNTFPDLNVLVSFLYSSD 239  
Db 181 LHYLOVNSTISVRVDFQYVDTNTFPDLNVLVSFLYSSD 220

## RESULT 8

US-09-079-785-19  
; Sequence 19, Application US/09079785  
; Patent No. 6143869  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 6143869el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/079,785  
; FILING DATE:

; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 19:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 220 amino acids  
; TYPE: amino acid

; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-079-785-19

Query Match 91.6%; Score 1141; DB 4; Length 220;  
Best Local Similarity 100.0%; Pred. No. 3.2e-106;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 20 MQVQPGSVASPRSTRPWRSTSRYSFYLTALVCLVAVAILLVVQKDKDSTPNTTEK 79  
Db 1 MQVQPGSVASPRSTRPWRSTSRYSFYLTALVCLVAVAILLVVQKDKDSTPNTTEK 60  
Qy 80 APLKGGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTTHGLIYQDGNLIQV 139  
Db 61 APLKGGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTTHGLIYQDGNLIQV 120  
Qy 140 FPLGLFYVQQLQFLVQCSNHSVDLTLLQLLNSKIKKQTLVTVCSGVQSKNIYQNLQFL 199  
Db 121 FPLGLFYVQQLQFLVQCSNHSVDLTLLQLLNSKIKKQTLVTVCSGVQSKNIYQNLQFL 180  
Qy 200 LHYLVQNSTISVRVDFQVVDNTFPDLNVLVSFLYSSSD 239  
Db 181 LHYLVQNSTISVRVDFQVVDNTFPDLNVLVSFLYSSSD 220

RESULT 9  
US-08-225-989-8  
; Sequence 8, Application US/08225989  
; Patent No. 5480981  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E

; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 234 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-225-989-8

Query Match 69.1%; Score 860.5; DB 1; Length 234;  
Best Local Similarity 69.6%; Pred. No. 3.3e-78;  
Matches 167; Conservative 28; Mismatches 38; Indels 7; Gaps 2;  
Qy 1 MEPGLQAGSCGAPSPDPAMQVQPGSVASPRSTRPWRSTSRYSFYLTAL-VCLVAV 59  
Db 1 MDPGLQALNGMAPGPDAMHVPAGSVAS-----HLGTTSRYSFYLTATLALCLVFTV 54  
Qy 60 AILVLVQKDKDSTPNTTEKAPLKGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLS 119  
Db 55 ATIMVLVQRTDSIPNSPDNVPKGGNCSEDLCLIKRAPFKSWAYLQVAKHLNNTKLS 114  
Qy 120 WNEDGTTHGLIYQDGNLIYQVFPGLFYVQQLQFLVQCSNHSVDLTLLQLLNSKIKKQTLV 179  
Db 115 WNKDGLHGVRYQDGNLIYQVFPGLFYIICQLQFLVQCPNNSVDLLELLINKHIKKQALV 174  
Qy 180 TVCESGVQSKNIYQNLQFLHLYLVQVNSTISVRVDFQVVDNTFPDLNVLVSFLYSSSD 239  
Db 175 TVCESGMQTKHYVQNLQFLDYLVQNTTISVNVDTFQYIDTSTFPLENVLSIFLYSNSD 234

RESULT 10  
US-08-570-923-8  
; Sequence 8, Application US/08570923  
; Patent No. 5677430  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/570,923  
; FILING DATE: 12-DEC-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992

G DATE: 12 APRIL 1994  
CATION NUMBER: US 07/966,775  
G DATE: 27-OCT-1992  
IFICATION: 530  
PLICATION DATA:  
CATION NUMBER: US 907,224  
G DATE: 01-JUL-1992  
APPLICATION DATA:  
CATION NUMBER: US 899,660  
G DATE: 15-JUN-1992  
PLICATION DATA:  
CATION NUMBER: US 892,459  
G DATE: 02-JUN-1992  
APPLICATION DATA:  
CATION NUMBER: US 889,717  
G DATE: 26-MAY-1992  
AGENT INFORMATION:  
Seese, Kathryn A.  
TRATION NUMBER: 32,172  
ENCE/DOCKET NUMBER: 2804-E  
MUNICATION INFORMATION:  
HONE: (206)587-0430  
AX: (206)233-0644  
: 756822  
ON FOR SEQ ID NO: 8:  
E CHARACTERISTICS:  
H: 234 amino acids  
amino acid  
OGY: linear  
E TYPE: protein  
4-8

69.1%; Score 860.5; DB 1; Length 234;  
Similarity 69.6%; Pred.No. 3.3e-78;  
67; Conservative 28; Mismatches 38; Indels 7; Gaps 2;  
PGLPGIQQAGSGCGSPDAMQVPGSVASPWRSRSTSRSYFLSTTAL-VCLWVAW 59  
||||| : || | || | || | || | || | || | || | || | || |  
: || | || | || | || | || | || | || | || | || |  
PGLPGIQQALNGMAPGCDTAMHPACSVAS-----HLGTTSSRYFLTATLALCLFTV 54  
||||| : || | || | || | || | || | || | || | || | || |  
: || | || | || | || | || | || | || | || | || |  
ILVLVVOKKSDPTNTTEKAPLKGGNCSEDLFCTLKSTPSKKSWAYLOVSKHLNNTKLS 119  
||||| : || | || | || | || | || | || | || | || | || |  
IMLVVVQRTDSIPNSPDNVPLKGGNCSEDLCLIKRAPFKKSWAYLOVAKHLNKTLS 114  
||| : || | || | || | || | || | || | || | || | || |  
EDGTGTHGLYQDNLIVQFFGLFYFCQLQFLVQCNSHNSVDLTLLQLINSIKKOTLV 179  
||| : || | || | || | || | || | || | || | || | || |  
KDQILGHGVYQDGNLVQFFGLFYICQLQFLVQCPNNSVDLKLLELINHKIKOALV 174  
||| : || | || | || | || | || | || | || | || | || |  
CESGVGSKNITQNLSQFLHLHYLVNSTISVRVDNFQVDTNTPFDNLVSFLYSDD 239  
||| : || | || | || | || | || | || | || | || | || |  
CESGMOTKHVYNLSQFLDYLVQNTISVNVTFOYIDISTFPLENVLSIFLYSNSD 234  
||| : || | || | || | || | || | || | || | || | || |

5-8  
Application US/09079785  
6143869  
INFORMATION:  
NT: Goodwin, Raymond G.  
NT: Smith, Craig A.  
NT: Armitage, Richard J.  
NT: Gruss, Hans-Jürgen  
F INVENTION: No. 6143869el Cytokine That Binds CD30  
OF SEQUENCES: 23  
CONDENCE ADDRESS:  
SSEE: Kathryn A. Seese, Immunex Corporation  
T: 51 University Street  
Seattle  
: Washington  
RY: USA  
98101  
READABLE FORM:

G DATE: 12 APRIL 1994  
CATION NUMBER: US 07/966,775  
G DATE: 27-OCT-1992  
IFICATION: 530  
PLICATION DATA:  
CATION NUMBER: US 907,224  
G DATE: 01-JUL-1992  
APPLICATION DATA:  
CATION NUMBER: US 899,660  
G DATE: 15-JUN-1992  
PLICATION DATA:  
CATION NUMBER: US 892,459  
G DATE: 02-JUN-1992  
APPLICATION DATA:  
CATION NUMBER: US 889,717  
G DATE: 26-MAY-1992  
Y/AGENT INFORMATION:  
Seese, Kathryn A.  
TRATION NUMBER: 32,172  
ENCE/DOCKET NUMBER: 2804-E  
MUNICATION INFORMATION:  
HONE: (206)587-0430  
AX: (206)233-0644  
: 756822  
ON FOR SEQ ID NO: 8:  
E CHARACTERISTICS:  
H: 234 amino acids  
amino acid  
OGY: linear  
E TYPE: protein  
4-8

h  
67; Similarity 69.1%; Score 860.5; DB 1; Length 234;  
Conservative 28; Mismatches 38; Indels 7; Gaps 2;

PPGLQQAGSGCAPSPDAMQVPGSVASPWSTRSFYFLSTTAL-VCLWVAW 59  
||||| : || ||||| : ||||| : ||||| : ||||| :  
PPGLQQALNGMAPGCDTAMHPACSVAS-----HLGTTSRSYFLTATLALCLFTV 54  
||||| : || ||||| : ||||| : ||||| : ||||| :  
ILVLVVOKKSDPTNTTEKAPLKGGNCSEDLFCTLKSTPSKKSWAYLOVSKHLNNTKLS 119  
||||| : ||||| : ||||| : ||||| : ||||| :  
IMLVVVQRTDSIPNSPDNVPLKGGNCSEDLCLIKRAPFKKSWAYLOVAKHLNKTLS 114  
EDGTGHGLIYODNLIVQFFGLFIYICQLQFLVQCNSHSDLTLLQLINSIKIKOTLV 179  
:||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :  
KDGIHLGVRYQDGNLVIQFFGLFIYICQLQFLVQCNPNSVDLKLLELLINKHIKQALV 174  
CESGVGSKNITQNLSOFLHLHYLVNSTISVRVDNFQVDTNTPFDNLVSFLYSDD 239  
:||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :  
CESGMOTKHVYNLSQFLDYLVQNTTISVNVDTFQIDISTFPLENVLSIFLYSNSD 234

5-8  
Application US/09079785  
6143869  
INFORMATION:  
NT: Goodwin, Raymond G.  
NT: Smith, Craig A.  
NT: Armitage, Richard J.  
NT: Gruss, Hans-Jürgen  
P INVENTION: No. 6143869el Cytokine That Binds CD30  
OF SEQUENCES: 23  
CONDENCE ADDRESS:  
SSEE: Kathryn A. Seese, Immunex Corporation  
T: 51 University Street  
Seattle  
: Washington  
RY: USA  
98101  
READABLE FORM:

G DATE: 12 APRIL 1994  
CATION NUMBER: US 07/966,775  
G DATE: 27-OCT-1992  
IFICATION: 530  
PLICATION DATA:  
CATION NUMBER: US 907,224  
G DATE: 01-JUL-1992  
APPLICATION DATA:  
CATION NUMBER: US 899,660  
G DATE: 15-JUN-1992  
PLICATION DATA:  
CATION NUMBER: US 892,459  
G DATE: 02-JUN-1992  
APPLICATION DATA:  
CATION NUMBER: US 889,717  
G DATE: 26-MAY-1992  
Y/AGENT INFORMATION:  
Seese, Kathryn A.  
TRATION NUMBER: 32,172  
ENCE/DOCKET NUMBER: 2804-E  
MUNICATION INFORMATION:  
HONE: (206)587-0430  
AX: (206)233-0644  
: 756822  
ON FOR SEQ ID NO: 8:  
E CHARACTERISTICS:  
H: 234 amino acids  
amino acid  
OGY: linear  
E TYPE: protein  
4-8

h  
67; Similarity 69.1%; Score 860.5; DB 1; Length 234;  
Conservative 28; Mismatches 38; Indels 7; Gaps 2;

PPGLQQAGSGCAPSPDAMQVPGSVASPWRSRSTSRSYFLSTTAL-VCLWVAW 59  
||||| : || ||||| : ||||| : ||||| : ||||| :  
PPGLQQALNGMAPGCDTAMHPACSVAS-----HLGTTSSRYFLTATLALCLFTV 54  
||||| : || ||||| : ||||| : ||||| : ||||| :  
ILVLVVOKKSDPTNTEKAPLKGGNCSEDLFCTLKSTPSKKSWAYLVQVSKHLNNTKLS 119  
||||| : ||||| : ||||| : ||||| : ||||| :  
IMVLVVQRTDSIPNSPDNVPLKGGNCSEDLCLIKRAPFKKSWAYLVQAKHLNKTLS 114  
EDGTGHGLIYODNLIVQFFGLFYFCQLQFLVQCNSHSDLTLLQLINSIKIKQTLV 179  
:||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :  
KDGIHLGVYQDGNLVQIFPFGLYFIQQLQFLVQCPNNSVDLKLLELLINKHIKQALV 174  
CESGVGSKNITQNLSOFLHLHYLVNSTISVRVDNFQVDTNTPFDNLVSFLYSDD 239  
:||| : ||||| : ||||| : ||||| : ||||| : ||||| : ||||| :  
CESGMOTKHVYNLSQFLLDYLQVNTTISVNVDTFQIDISTFPLENVLSIFLVSND 234

5-8  
Application US/09079785  
6143869  
INFORMATION:  
NT: Goodwin, Raymond G.  
NT: Smith, Craig A.  
NT: Armitage, Richard J.  
NT: Gruss, Hans-Jürgen  
F INVENTION: No. 6143869el Cytokine That Binds CD30  
OF SEQUENCES: 23  
CONDENCE ADDRESS:  
SSEE: Kathryn A. Seese, Immunex Corporation  
T: 51 University Street  
Seattle  
: Washington  
RY: USA  
98101  
READABLE FORM:



;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: Apple Macintosh  
;; OPERATING SYSTEM: Apple 7.1  
;; SOFTWARE: Microsoft Word, Version 5.1a  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/079,785  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/225,989  
;; FILING DATE: 12 APRIL 1994  
;; APPLICATION NUMBER: US 07/966,775  
;; FILING DATE: 27-OCT-1992  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 907,224  
;; FILING DATE: 01-JUL-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 899,660  
;; FILING DATE: 15-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 892,459  
;; FILING DATE: 02-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 889,717  
;; FILING DATE: 26-MAY-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Seese, Kathryn A.  
;; REGISTRATION NUMBER: 32,172  
;; REFERENCE/DOCKET NUMBER: 2804-E  
;; TELEPHONE: (206)587-0430  
;; TELEFAX: (206)233-0644  
;; TELEX: 756822  
;; INFORMATION FOR SEQ ID NO: 8:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 234 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-09-079-785-8

Query Match 69.1%; Score 860.5; DB 4; Length 234;  
Best Local Similarity 69.6%; Pred. No. 3.3e-78;  
Matches 167; Conservative 28; Mismatches 38; Indels 7; Gaps 2;

Qy 1 MEPGLQQAGSCAPSPDPAMQVQGSVSPWRSTSRYSFYLSLTAL-VCLVAV 59  
Db 1 MDPGLQQALNGMAPPGDTAMHVPAGSVAS-----HLGTTSRYSFYLTATLALCLVFTV 54  
Qy 60 AILVLVQKDKSTPTNTTEKAPLKGNCSEDLFCTLKSTPKSKSWAYLOVSKHLNNTKLS 119  
Db 55 ATIMVLVQRTDSIPNSPDNPVPLKGNCSEDLILKRAPFKSKSWAYLOVAKHLNNTKLS 114  
Qy 120 WNEGTTHGLIYQDGNLIYQFGLFIYVQGLFVQCSNHSVDLTQLLINSKIKKQTLV 179  
Db 115 WNKDGLHGVRYQDGNLIYQFGLFIYVQGLFVQCSNHSVDLTQLLINSKIKKQALV 174  
Qy 180 TVCESGVQSKNIYQNLQSOFLHLYQVNSTISVRVDFNQVYDNTFPDNLVSLVSSD 239  
Db 175 TVCESGMOTKHVYQNLQSOFLDLYQVNTTISVNDTFQYIDTSTFPLENVLSIFLYSNSD 234

RESULT 13  
US-08-225-989-23  
; Sequence 23, Application US/08225989  
; Patent No. 5480981  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen

;; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30  
;; NUMBER OF SEQUENCES: 23  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
;; STREET: 51 University Street  
;; CITY: Seattle  
;; STATE: Washington  
;; COUNTRY: USA  
;; ZIP: 98101  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: Apple Macintosh  
;; OPERATING SYSTEM: Apple 7.1  
;; SOFTWARE: Microsoft Word, Version 5.1a  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/225,989  
;; FILING DATE: 12 APRIL 1994  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 907,224  
;; FILING DATE: 01-JUL-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 899,660  
;; FILING DATE: 15-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 892,459  
;; FILING DATE: 02-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 889,717  
;; FILING DATE: 26-MAY-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Seese, Kathryn A.  
;; REGISTRATION NUMBER: 32,172  
;; REFERENCE/DOCKET NUMBER: 2804-E  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206)587-0430  
;; TELEFAX: (206)233-0644  
;; TELEX: 756822  
;; INFORMATION FOR SEQ ID NO: 23:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 215 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-225-989-23

Query Match 65.4%; Score 814.5; DB 1; Length 215;  
Best Local Similarity 70.8%; Pred. No. 1.1e-73;  
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

Qy 20 MQVQPGSVASPWSTSRYSFYLSLTAL-VCLVAVAILVLVQVKDSTPTTE 78  
Db 1 MHPVAGSVAS-----HLGTTSRYSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPD 54  
Qy 79 KAPLKGNCSEDLFCTLKSTPKSKSWAYLOVSKHLNNTKLSWNEGTTHGLIYQDGNLIY 138  
Db 55 NVPLKGNCSEDLILKRAPFKSKSWAYLOVAKHLNNTKLSWNEGTTHGLIYQDGNLIY 114  
Qy 139 QFGLFIYVQGLFVQCSNHSVDLTQLLINSKIKKQTLVTVCESGVQSKNIYQNLQSO 198  
Db 115 QFGLFIYVQGLFVQCSNHSVDLTQLLINSKIKKQALVTVCESGMOTKHVYQNLQSO 174  
Qy 199 LHYQVNSTISVRVDFNQVYDNTFPDNLVSLVSSD 239  
Db 175 LDYLVQVNTTISVNDTFQYIDTSTFPLENVLSIFLYSNSD 215

RESULT 14

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Qy 139 QPGLYFIVCOLQFLVOCVSHSVSDTLTQLLNSIKKQTLVTVCESGVQSKNIYQNLQSF 174
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Db 115 QPGLYFIIICQLQFLVQCPNNSVDLKLKELLINKIKKQALVTVCESGMQTKHVYQNLQSF 174
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 199 LLHYLVNSTISVRDVFQVYDVTNTEPLDNLVSLVFLYSSSD 239
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 175 LDYLVNTTISVNDVTFQYIDTSTFFPLENVLISFLYSNSD 215
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RESULT 15
US-08-580-014-23
; Sequence 23, Application US/08580014
; Patent No. 5753203
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jürgen
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,014
; FILING DATE: 20-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-580-014-23

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Query Match 65.4%; Score 814.5; DB 1; Length 215;  
Best Local Similarity 70.6%; Pred. No. 1.1e-73;

Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

QY 20 MQVPGSVASPMWRSTRPWRSTSRSYFYLSTAL-VCLVAVAILVLVQVKDSTPNTTE 78  
 Db 1 MHVPAGSVAS-----HLGTTSSRSYFYLTTATLALCLVFTVATIMVLVQVQTDSPNSPD 54

QY 79 KAPLKGNCSEDLFCITLKSTPKSWAYLQVSKHLNNTKLSWNEEDGTIHLIYODGNLIV 138  
 Db 55 NVPLKGGNCSEDLILKRAPEKSWAYLQVAKHLNNTKLSWNEEDGTIHLIYODGNLIV 114

QY 139 OPFGLYFIVCOLQFLVQCSNHSVDLTLOLLINSKIKKOTLVTVCESGVQSKNIYQNLQF 198  
 Db 115 QPGLYFIIICQLQFLVQCPNNSVDLLELLINKHKKQALVTVCESGMQTKHYQNLQF 174

QY 199 LLHYLQVNSTISVRVDNFQYVDNTFPLDNVLSVFLYSSSD 239  
 Db 175 LLDYLQVNTTISVNVDTFOYIDTSTPLENVLSIFLYSNSD 215

Search completed: September 5, 2001, 10:23:10  
 Job time: 85 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2001, 10:21:45 ; Search time 44.86 Seconds  
(without alignments)  
322.986 Million cell updates/sec

Title: US-09-628-126-6  
Perfect score: 1246  
Sequence: 1 MEPLQAGSCGAPSPDPAM.....DTNTPFLDNLSVFLYSSD 239

Scoring table:  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_0601:\*  
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2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT:\*  
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17: /SID88/gcgdata/geneseq/geneseq/AA1996.DAT:\*  
18: /SID88/gcgdata/geneseq/geneseq/AA1997.DAT:\*  
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20: /SID88/gcgdata/geneseq/geneseq/AA1999.DAT:\*  
21: /SID88/gcgdata/geneseq/geneseq/AA2000.DAT:\*  
22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1246	100.0	239	14 AAR45008	Sequence encoded b
2	1141	91.6	220	14 AAR45006	Sequence encoded b
3	860.5	69.1	234	14 AAR45009	Sequence encoded b
4	814.5	65.4	215	14 AAR45007	Sequence encoded b
5	742	59.6	143	21 AAB08277	Amino acid sequenc
6	600	48.2	143	21 AAB08276	Amino acid sequenc
7	126	10.1	279	17 AAB88357	Mouse Fas ligand.
8	123	9.9	279	16 AAR79098	Mouse Fas ligand.
9	110	8.8	279	16 AAR77282	Mouse Fas-L protei
10	109	8.7	179	16 AAR79069	Mouse Fas ligand (
11	102	8.2	278	16 AAR79095	Rat Fas ligand enc

12	102	8.2	278	20 AAW98069	Rat Fas ligand (Fa
13	102	8.2	278	20 AAW95040	Rat FasL protein.
14	97	7.8	138	16 AAR79068	Mouse Fas ligand (
15	97	7.8	143	21 AAB08266	Amino acid sequenc
16	95.5	7.7	258	20 AAY04371	Human Fas ligand d
17	95	7.6	137	16 AAR79067	Mouse Fas ligand (
18	92	7.4	271	20 AAR78596	Fas ligand (FasL)
19	91	7.3	179	16 AAR79066	Rat Fas ligand (pa
20	91	7.3	309	18 AAR64189	Murine 4-1BB-L pol
21	91	7.3	309	18 AAW26656	Murine 4-1BB ligand
22	89.5	7.2	268	19 AAW48953	Non-cleavable Fas
23	88.5	7.1	448	21 AAB28694	Fc-muAGP-1 (99-291
24	88	7.1	281	20 AAY04373	Human Fas ligand d
25	88	7.1	281	21 AAY87576	Human Fas ligand (
26	88	7.1	281	21 AAY87581	Human Fas ligand (
27	87	7.0	265	19 AAW48954	Non-cleavable Fas
28	87	7.0	277	20 AAY04372	Human Fas ligand d
29	87	7.0	281	16 AAR77281	Human Fas-L protei
30	87	7.0	281	16 AAR79097	Human Fas ligand.
31	87	7.0	281	17 AAR98104	Human Fas ligand d
32	87	7.0	281	17 AAR88356	Human Fas ligand.
33	87	7.0	281	18 AAW27143	Human Fas ligand.
34	87	7.0	281	19 AAW75959	Human Fas ligand.
35	87	7.0	281	19 AAW49105	Fas Ligand. Mamma
36	87	7.0	281	20 AAY28594	Wild type Fas liga
37	87	7.0	281	20 AAW98071	Human Fas ligand (
38	87	7.0	281	20 AAW95041	Human FasL protein
39	87	7.0	281	21 AAB19342	Amino acid sequenc
40	87	7.0	281	21 AAY87569	Human Fas ligand (
41	87	7.0	281	21 AAY87577	Human Fas ligand (
42	87	7.0	281	21 AAY87578	Human Fas ligand (
43	87	7.0	281	21 AAY87579	Human Fas ligand (
44	87	7.0	281	21 AAY87582	Human Fas ligand (
45	87	7.0	2013	21 AAB18265	Plasmodium falcipa

## ALIGNMENTS

RESULT 1  
AAR45008  
ID AAR45008 standard; Protein; 239 AA.  
XX  
AC AAR45008;  
XX  
DT 19-JUN-1994 (first entry)  
XX  
DE Sequence encoded by a murine CD30-L cDNA clone  
DE encoding additional N-terminal amino acids.  
XX  
KW Hodgkin's disease; lymphoma; surface antigen; cytokine;  
KW CD30 ligand; CD30-L; TNF; NGF.  
XX  
OS Acromys cahirinus.  
XX  
FH Key Location/Qualifiers  
FT Region 47..67  
FT Transmembrane /label-  
XX  
PN WO9324135-A.  
XX  
PD 09-DEC-1993.  
XX  
PF 25-MAY-1993; 93WO-US04926.  
XX  
PR 26-MAY-1992; 92US-0889717.  
PR 02-JUN-1992; 92US-0892459.  
PR 15-JUN-1992; 92US-0899660.  
PR 01-JUL-1992; 92US-0907224.  
PR 27-OCT-1992; 92US-0966775.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX

PI Armitage RJ, Goodwin RG, Smith CA;

DR WPI; 1993-405417/50.

DR N-PSDB; AAQ53537.

XX New cytokine, CD30-L, which binds CD30 - used for developing  
PT prods. for diagnosis, detection, purifications, research and  
PT therapy

PS Claim 15; Figure 6a; 59pp; English.

XX CD30-L is a ligand for CD30, the 120kd surface antigen widely used  
CC as a clinical marker for Hodgkin's lymphoma and related haematologic  
CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-  
CC L and other derived prods. can be used for elucidating the roles  
CC that CD30 and CD30-L may play in the immune system and for diagnosis  
CC and therapy. It can be isolated as follows. A cDNA library prepd from  
CC the murine helper T-cell line 7B9 is screened with a CD30/FC fusion  
CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L  
CC (AAQ53535). This cDNA can then be used as a probe to screen a human PBL  
CC cDNA library to obtain cDNA encoding human CD30-L (AAQ53536). An  
CC anchored PCR technique was employed to isolate CD30-L human and murine  
CC clones containing an additional 19 N-terminal amino acid sequence  
CC (AAQ53537, AAQ53538).

XX Sequence 239 AA;

Query Match 100.0%; Score 1246; DB 14; Length 239;  
Best Local Similarity 100.0%; Pred. No. 1.4e-116;  
Matches 239; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MEGLIQAGSGCAPSPDPAMQVPGSVASGPRSTRPWRSTRSYFYLTALVCLVAVVA 60  
Db {}  
Qy 1 MEGLIQAGSGCAPSPDPAMQVPGSVASGPRSTRPWRSTRSYFYLTALVCLVAVVA 60  
Db {}  
Qy 61 IILVLVQKOSTPNTTEKAPLKGNCSEDLFTLSTPSKKSWAYLQVSKHLNNTKLSW 120  
Db 61 IILVLVQKOSTPNTTEKAPLKGNCSEDLFTLSTPSKKSWAYLQVSKHLNNTKLSW 120  
Qy 121 NEDGTIHLGLIYQDGNLIYVQFGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVT 180  
Db 121 NEDGTIHLGLIYQDGNLIYVQFGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVT 180  
Qy 181 VCESGVQSKNIYQNLQSFLLHVLQVNSTISVRVDNFQYVDTNFTPLDNVLSVFLYSSSD 239  
Db 181 VCESGVQSKNIYQNLQSFLLHVLQVNSTISVRVDNFQYVDTNFTPLDNVLSVFLYSSSD 239

RESULT 2

AAR45006  
ID AAR45006 standard; Protein; 220 AA.

XX AAR45006;

DT 19-JUN-1994 (first entry)

DE Sequence encoded by a murine CD30-L cDNA clone.

XX Hodgkin's disease; lymphoma; surface antigen; cytokine;  
KW CD30 ligand; CD30-L; TNF; NGF.

XX Acomys cahirinus.

XX Key Location/Qualifiers  
FH Region 28..48  
FT /label= transmembrane

XX WO9324135-A.

XX 09-DEC-1993.

XX 25-MAY-1993; 93WO-US04926.

XX 26-MAY-1992; 92US-0889717.  
PR 02-JUN-1992; 92US-0892459.  
PR 15-JUN-1992; 92US-0899660.  
PR 01-JUL-1992; 92US-0907224.  
PR 27-OCT-1992; 92US-0966775.  
XX (IMMV ) IMMUNEX CORP.  
PA Armitage RJ, Goodwin RG, Smith CA;

XX WPI; 1993-405417/50.  
DR N-PSDB; AAQ53535.

XX New cytokine, CD30-L, which binds CD30 - used for developing  
PT prods. for diagnosis, detection, purifications, research and  
PT therapy

XX Claim 15; Figure 3a; 59pp; English.

CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used  
CC as a clinical marker for Hodgkin's lymphoma and related haematologic  
CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-  
CC L and other derived prods. can be used for elucidating the roles  
CC that CD30 and CD30-L may play in the immune system and for diagnosis  
CC and therapy. It can be isolated as follows. A cDNA library prepd from  
CC the murine helper T-cell line 7B9 is screened with a CD30/FC fusion  
CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L.  
CC This cDNA can then be used as a probe to screen a human PBL cDNA  
CC library to obtain cDNA encoding human CD30-L.

XX Sequence 220 AA;

Query Match 91.6%; Score 1141; DB 14; Length 220;  
Best Local Similarity 100.0%; Pred. No. 3.9e-106;  
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 MQVOPGVSASPRSTRPWRSTRSYFYLTALVCLVAVAIILVLVYQKSDSTPTTEK 79  
Db 1 mqvpgsvasprstrpwrstrsyfyllsttalvclvvavaiilvlvqqkdstptttek 60  
Qy 80 APLKGGNCSEDLFTLSTPSKKSWAYLQVSKHLNNTKLSWNEDGTIHLIYQDGNLIYQ 139  
Db 61 aplkggncsedlftlktstpskkswaylqvskhlntklswnedgtibglyqdgndliyv 120  
Qy 140 FPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVTVCSGVQSKNIYQNLQSF 199  
Db 121 fpglyfivcqlqflvqcsnhsvdltqlllnskkkqtlvtvcsesgvqskniyqnlsgfl 180  
Qy 200 LHYLQVNSTISVRVDNFQYVDTNFTPLDNVLSVFLYSSSD 239  
Db 181 lhyiqvnstisvrvdnfyvdtntfcpldnvlsvflysssd 220

RESULT 3

AAR45009  
ID AAR45009 standard; Protein; 234 AA.

XX AAR45009;

DT 19-JUN-1994 (first entry)

DE Sequence encoded by a human CD30-L cDNA clone  
DE encoding additional N-terminal amino acids.

XX Hodgkin's disease; lymphoma; surface antigen; cytokine;  
KW CD30 ligand; CD30-L; TNF; NGF.

XX Homo sapiens.

XX Key Location/Qualifiers  
FH Region 41..62

FT XX /label= Transmembrane

PN WO9324135-A.

PD 09-DEC-1993.

XX 25-MAY-1993; 93WO-US04926.

XX 26-MAY-1992; 92US-0889717.

PR 02-JUN-1992; 92US-0892459.

PR 15-JUN-1992; 92US-0899660.

PR 01-JUL-1992; 92US-0907224.

PR 27-OCT-1992; 92US-0966775.

XX (IMMV ) IMMUNEX CORP.

PI Armitage RJ, Goodwin RG, Smith CA;

DR WPI: 1993-405417/50.

DR N-PSDB; AAQ53538.

XX New cytokine, CD30-L, which binds CD30 - used for developing

PT prods. for diagnosis, detection, purifications, research and

PT therapy

XX Claim 15; Figure 7a; 59pp; English.

XX CD30-L is a ligand for CD30, the 120kd surface antigen widely used  
CC as a clinical marker for Hodgkin's lymphoma and related haematologic  
CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-  
CC L and other derived prods. can be used for elucidating the roles  
CC that CD30 and CD30-L may play in the immune system and for diagnosis  
CC and therapy. It can be isolated as follows. A cDNA library prepd. from  
CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion  
CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L  
CC (AAQ53535). This cDNA can then be used as a probe to screen a human PBL  
CC cDNA library to obtain cDNA encoding human CD30-L (AAQ53536). An  
CC anchored PCR technique was employed to isolate CD30-L human and murine  
CC clones containing an additional 19 N-terminal amino acid sequence  
CC (AAQ53537, AAQ53538).

XX Sequence 234 AA;

Query Match 69.1%; Score 860.5; DB 14; Length 234;  
Best Local Similarity 69.6%; Pred. No. 4.6e-78;  
Matches 167; Conservative 28; Mismatches 38; Indels 7; Gaps 2;

QY 1 MPEGLQAGSCGAPDPDPAQVQPGSVASWPRSRSTSRFYLSLTTAL-VCLVAV 59

Db 1 mdpglqalngmappgdgtamhvpagsvas-----hlggttsrsyfittatlaclvftv 54

QY 60 AIIILVAVOKDSTPNTTEKAPLKGNCSEDLCTLKSTPSKSWAYLOVSKHLNNTKLS 119

Db 55 atimvlvtdtsipnsdpnvpkgncsedllcilkrapfkkswaylqvakhnktkls 114

QY 120 WNEDEGTIHLIYQDGNLIYQFPGLYIVCOQLVQCSNHSVDLTQLLINSKIKKQTLV 179

Db 115 wnkdgilhvrygdgnlvqfpglyfiicqlqlvqcpnnsvdiklellinkhkhkqalv 174

QY 180 TVCESGVQSKNIYONISQELLLHYLQVNSTISVRVDFNFTFPDLNLSVFLYSSD 239

Db 175 tvcesgmqtkhvygnlsqfildylqvnvttsvndtftgtdstfplenvlsiflynsd 234

RESULT 4

AAR45007

ID AAR45007 standard; Protein; 215 AA.

XX AAR45007;

XX 19-JUN-1994 (first entry)

XX

DE Sequence encoded by a human CD30-L cDNA clone.  
XX Hodgkin's disease; lymphoma; surface antigen; cytokine;  
KW CD30 ligand; CD30-L; TNF; NGF.  
XX Homo sapiens.

OS

EH Key Location/Qualifiers  
FT Region 22..43  
FT /label= transmembrane

PN WO9324135-A.

XX 09-DEC-1993.

XX 25-MAY-1993; 93WO-US04926.

XX 26-MAY-1992; 92US-0889717.

PR 02-JUN-1992; 92US-0892459.

PR 15-JUN-1992; 92US-0899660.

PR 01-JUL-1992; 92US-0907224.

PR 27-OCT-1992; 92US-0966775.

XX (IMMV ) IMMUNEX CORP.

PI Armitage RJ, Goodwin RG, Smith CA;

DR WPI: 1993-405417/50.

DR N-PSDB; AAQ53536.

XX New cytokine, CD30-L, which binds CD30 - used for developing

PT prods. for diagnosis, detection, purifications, research and

PT therapy

XX Claim 15; Figure 5a; 59pp; English.

XX CD30-L is a ligand for CD30, the 120kd surface antigen widely used  
CC as a clinical marker for Hodgkin's lymphoma and related haematologic  
CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-  
CC L and other derived prods. can be used for elucidating the roles  
CC that CD30 and CD30-L may play in the immune system and for diagnosis  
CC and therapy. It can be isolated as follows. A cDNA library prepd. from  
CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion  
CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L.  
CC This cDNA can then be used as a probe to screen a human PBL cDNA  
CC library to obtain cDNA encoding human CD30-L.

XX Sequence 215 AA;

Query Match 65.4%; Score 814.5; DB 14; Length 215;  
Best Local Similarity 70.6%; Pred. No. 1.6e-73;  
Matches 156; Conservative 26; Mismatches 33; Indels 7; Gaps 2;

QY 20 MOVQPGSVASWPRSRSTSRFYLSLTTAL-VCLVAVAILLVVQKDKSTPNTTE 78

Db 1 mhvpagsvas-----hlggttsrsyfittatlaclvftvatimlvvqtdtsipnsd 54

QY 79 KAPLKGNCSEDLCTLKSTPSKSWAYLOVSKHLNNTKLSWNEDEGTIHLIYQDGNLIV 138

Db 55 nvplkgncsedllcilkrapfkkswaylqvakhnktklswnkdgilhvryqgdnivi 114

QY 139 QPFGLYFIVCOQLVQCSNHSVDLTQLLINSKIKKQTLVTVCSGVQSKNIYONLSQF 198

Db 115 qfpglyfiicqlqlvqcpnnsvdiklellinkhkhkqalvctcesgmqtkhvygnlsqf 174

QY 199 LLHYLQVNSTISVRVDFNFTFPDLNLSVFLYSSD 239

Db 175 lldylqvnvttsvndtftgtdstfplenvlsiflynsd 215

RESULT 5

AAB08277

ID	AA08277	standard; Protein; 143 AA.
XX	XX	
AC	AA08277;	
XX	XX	
DT	04-DEC-2000	(first entry)
XX	XX	
DE	Amino acid sequence of a mouse TNF ligand CD30L.	
XX	XX	
KW	AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;	
KW	type II transmembrane protein; B cell stimulatory factor;	
KW	inflammatory disorder; immune disorder; rheumatoid arthritis;	
KW	lupus and graft versus host disease.	
XX	XX	
OS	Mus sp.	
XX	XX	
PN	W0200047740-A2.	
XX	XX	
PD	17-AUG-2000.	
XX	XX	
PF	11-FEB-2000; 2000WO-US03653.	
XX	XX	
PR	12-FEB-1999; 99US-0119906.	
PR	18-NOV-1999; 99US-0166271.	
XX	XX	
PA	(AMGE-) AMGEN INC.	
XX	XX	
PI	Boyle WJ, Hsu H;	
XX	XX	
DR	WPI; 2000-558217/51.	
XX	XX	
PT	Novel polypeptides comprising tumour necrosis factor ligand family	
PT	proteins, useful for treating inflammatory and immune disorders, e.g.	
PT	rheumatoid arthritis -	
XX	XX	
PS	Claim 14; Fig 9; 71pp; English.	
XX	XX	
CC	AA08265-83 represent tumour necrosis factor (TNF) ligands. The	
CC	specification describes an AGP-3 polypeptide, which is TNF ligand	
CC	family member. AGP-3 is a type II transmembrane protein, and is a	
CC	potent B cell stimulatory factor. Expression of AGP-3 correlates to	
CC	increases in the number of B cells and immunoglobulins produced.	
CC	AGP-3 proteins, antibodies, and nucleic acids may be used to treat	
CC	inflammatory and immune disorders, e.g. rheumatoid arthritis,	
CC	Crohn's disease, lupus and graft versus host disease. The nucleic	
CC	acids may be used to regulate the expression of an AGP-3 related	
CC	protein. The AGP-3 proteins, antibodies and nucleic acids are also	
CC	useful for the detection of AGP-3 agonists, antagonists and	
CC	characterizing interactions with AGP-3 related proteins.	
XX	XX	
SQ	Sequence 143 AA;	
	Query Match 59.6%; Score 742; DB 21; Length 143;	
	Best Local Similarity 100.0%; Pred. No. 1.6e-66;	
	Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps	
QY	97 STPSKSWAYLQYSKHLNNTKLSWNEDGTIHGIYODGNLIYQFGLYFIVCOLQFLVOC	156
Db	1 stpskswaylqyskhlhnnctklswnedgtihgiyodgnliyfpglyfivcqlqlfvcg	60
QY	157 SNHSVDLTQLLLNSKIKKOTLVTVCESGVQSKNIYONLSQFLLHYLQVNSTISVRDNF	216
Db	61 snhsvdltqlllnskkkqtlvtvcesgvqskniyqnlsgqllhylqvnstisvrndf	120
QY	217 QYVDNTNFPDLNLSVFLYSSSD	239
Db	121 qyvdtntfpdlndvlsflysssd	143
RESULT	6	
AA08276		
ID	AA08276	standard; Protein; 143 AA.
XX	XX	

AC	AAB08276;
XX	
DT	04-DEC-2000 (first entry)
XX	
DE	Amino acid sequence of a human TNF ligand CD30L.
XX	
KW	AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;
KW	type II transmembrane protein; B cell stimulatory factor;
KW	inflammatory disorder; immune disorder; rheumatoid arthritis;
KW	lupus and graft versus host disease.
XX	
OS	Homo sapiens.
XX	
PN	WO200047740-A2.
XX	
PD	17-AUG-2000.
XX	
PF	11-FEB-2000; 2000WO-US03653.
XX	
PR	12-FEB-1999; 99US-0119906.
PR	18-NOV-1999; 99US-0166271.
XX	
PA	(AMGE-) AMGEN INC.
XX	
PI	Boyle WJ, Hsu H;
XX	
DR	WPI; 2000-558217/51.
XX	
PT	Novel polypeptides comprising tumour necrosis factor ligand family
PT	proteins, useful for treating inflammatory and immune disorders, e.g.
PT	rheumatoid arthritis -
PS	Claim 14; Fig 9; 71pp; English.
XX	
CC	AAB08265-83 represent tumour necrosis factor (TNF) ligands. The
CC	specification describes an AGP-3 polypeptide, which is TNF ligand
CC	family member. AGP-3 is a type II transmembrane protein, and is a
CC	potent B cell stimulatory factor. Expression of AGP-3 correlates to
CC	increases in the number of B cells and immunoglobulins produced.
CC	AGP-3 proteins, antibodies, and nucleic acids may be used to treat
CC	inflammatory and immune disorders, e.g. rheumatoid arthritis,
CC	Crohn's disease, lupus and graft versus host disease. The nucleic
CC	acids may be used to regulate the expression of an AGP-3 related
CC	protein. The AGP-3 proteins, antibodies and nucleic acids are also
CC	useful for the detection of AGP-3 agonists, antagonists and
CC	characterizing interactions with AGP-3 related proteins.
XX	
SQ	Sequence 143 AA;
	Query Match 48.2%; Score 600; DB 21; Length 143;
	Best Local Similarity 77.3%; Pred. No. 2.6e-52;
	Matches 109; Conservative 19; Mismatches 13; Indels 0; Gaps
QY	99 PSKSWAYLOVSKHLNNTKLSDNGDTHGLIVODGNLI VQFPLGVICQLFLVQCNS 158
	:
Db	3 pfkkswaylvqakhlntklswndkgilhvrygdgnlvigfpglyfiqcqlgflvqcpn 62
	:
QY	159 HSVDLTLLQLINSKRKQTTLTVCESGVSQSNKYQNLSQFLLHYLQVNSTISVRVDNFQY 218
	:
Db	63 nsvdklelllnkhikgalvtvcsgmqtkhyqnlsqfilglylqymttisvnvdffqy 122
	:
QY	219 VDTWTFFLDNLVSFLYSDD 239
	:
Db	123 idtftplenvlisflynsd 143
	:
RESULT	7
AAR88357	
ID	AAR88357 standard; Protein: 279. AA.
XX	
AC	AAR88357;
XX	

```
Query Match          9.9%; Score 123; DB 16; Length 279;
Best Local Similarity 22.5%; Pred. Mismatches 0.0003;
Matches 55; Conservative 43; NoMatches 96; Indels 50; Gaps
Qy 10 SCG-----APSPDPMAMQVQGSVPWSTRTPRWSTRS-----YFYLSTTALV 53
      |||         |   |   |   |   |   |   |   |   |   |   |
Db 34 scqrqpdgrrrrrrrrppvpslpssqlplrlptlklkdkhtntnlwlvvfmmvalv 93
```





CC	the protein is a claimed Fas ligand able to induce apoptosis in
XX	cells which express the Fas cell surface antigen.
SQ	Sequence 278 AA;
	Query Match 8.2%; Score 102; DB 16; Length 278;
	Best Local Similarity 21.7%; Pred. No. 0.038;
	Matches 52; Conservative 37; Mismatches 105; Indels 46; Gaps 9;
QY	14 PSPDPAMQVPGSVASPWRSSTRPWRSTSRSYFYLLSTTALVCLVVAVAILL---VLVVOK 69
DB	47 pppppspippsqpppllpplsplkkkdnlelwlpiiffmvalvgmgymyqlflqlk 106
QY	70 KDSPTNTEKAPLKGGNCSEDLFCTLKSTPSK-----KSWAYLVQSKHLNNTKLSWNED-G 124
DB	107 elaelrefthslrvsfekqi--anpstsetkkprsvahltgnprsrslplewedyg 164
QY	125 T--IHGLIYDGNLIIVPPGLYFIYVCOQLFLVQCNS-----HSV-----DLTLQLL 168
DB	165 talisgvkykkgvilineaglyfyyskvyrfgscnsgplshkvmrnfkyppgdvlvIm-- 222
QY	169 INSKIKKQTILVTVCESGVQSCKNIYQNLSQFLHLYLVNSTISVRVDNFQVVDTNTPFLDN 228
DB	223 -----eekklnycttg-----qiwahssy'igavfnltcvadhlyvnislqlin 265
	RESULT 12
AAW98069	
ID	AAW98069 standard; Protein; 278 AA.
XX	AC AAW98069;
XX	AC AC
DT	21-JUN-1999 (first entry)
XX	Rat Fas ligand (FasL).
DE	
XX	FasL; Fas ligand; proinflammatory; immunosuppressive; rat;
KW	graft versus host disease; autoimmune disease; psoriasis;
KW	rheumatoid arthritis; systemic lupus erythematosus; gene therapy.
OS	Rattus sp.
XX	
Key	Location/Qualifiers
FT	Domain 78..99
FT	/note= "transmembrane domain"
FT	Modified-site 116
FT	/note= "N-glycosylated"
FT	Modified-site 130
FT	/note= "N-glycosylated"
FT	Modified-site 247
FT	/note= "N-glycosylated"
FT	Modified-site 257
FT	/note= "N-glycosylated"
XX	
PN	WO9903999-A1.
XX	
PD	28-JAN-1999.
XX	
PF	16-JUL-1998; 98WO-US14771.
PR	17-JUL-1997; 97US-0052829.
XX	(UNMI ) UNIV MICHIGAN.
PA	
PI	Chen J, Nabel GJ;
DR	WPI; 1999-132243/11.
DR	N-PSDB; AAX24877.
XX	
PT	Inhibition of proinflammatory responses - using an agent which
PT	modulates FasL stimulation, used for treating graft versus host
PT	disease or autoimmune disease

XX PS Disclosure; Fig 4A; 71pp; English.  
 CC This present sequence is rat Fas ligand (FasL). The invention  
 CC provides a method for inhibiting a proinflammatory response in a  
 CC cell mixture by administering an immunosuppressive agent which  
 CC inhibits the proinflammatory activity of FasL. In some embodiments,  
 CC FasL is coadministered with the immunosuppressive agent, and the  
 CC cell mixture comprises neutrophil cells. The method can be  
 CC practised in vitro, ex vivo or in vivo. Suitable immunosuppressive  
 CC agents include antisenescence molecules that inhibit endogenous FasL  
 CC expression, soluble Fas receptors or variants, ribozymes that  
 CC inhibit the endogenous expression of FasL, drugs that inhibit FasL  
 CC signalling, agents that induce the endogenous expression of  
 CC transforming growth factor (TGF)-beta, and polynucleotides coding  
 CC for an immunosuppressive agent such as TGF-beta. The method can be  
 CC used for treating diseases associated with an undesired FasL-mediated  
 CC proinflammatory response, e.g. graft versus host disease, or an  
 CC autoimmune disease such as systemic lupus erythematosus, rheumatoid  
 CC arthritis and psoriasis. The invention also provides a method for  
 CC identifying agents which modulate FasL stimulation of a  
 CC proinflammatory response.  
 XX SQ Sequence 278 AA;

Query Match 8.2%; Score 102; DB 20; Length 278;  
 Best Local Similarity 21.7%; Pred. No. 0.038;  
 Matches 52; Conservative 37; Mismatches 105; Indels 46; Gaps 9;  
 QY 14 PSPDPAMQVPGSVASPRSTRPWRSTRSRFYSLTALVCLVAVAILL----VLVVQK 69  
 Db 47 pppppspplppspqppplpplspkdkndielwlpviffmvalvgmglmyqlfhqk 106  
 QY 70 KDSPTNTEKAPLKGNCSEDLFCTLKSTPSK----KSWAYLQVSKHLNNTKLSWNED-G 124  
 Db 107 elaelrefthslrvssfekqi--anpstsetkkprsvahltgnprsrslplewedyg 164  
 QY 125 T--IHGLIYQDGNLIVQPGLYFIVCQLQFLVQCSN-----HSV-----DLTLQLL 168  
 Db 165 talisgvykkgglvineaglyfvyksvfyrgqscnspqshkvymrnfkypgdvlm-- 222  
 QY 169 INSKIKKQTLVTVCESGVQSKNIYQNLSQLFLHYLQVNSTISVRVDNFQYVDNTFPPLDN 228  
 Db 223 -----eeklnycttg-----qiwahssylgavfultvadhlyvnisqlslin 265

RESULT 13  
 AAW95040  
 ID AAW95040 standard; Protein; 278 AA.  
 XX AC AAW95040;  
 XX DT 14-MAY-1999 (first entry)  
 XX DE Rat FasL protein.  
 XX KW Cell proliferation; FasL protein; pathogen; modulation; cell locus;  
 XX KW proinflammatory response; inhibition; rat.  
 XX OS Rattus sp.  
 XX PN WO9903998-A1.  
 XX PD 28-JAN-1999.  
 XX PF 16-JUL-1998; 98WO-US14770.  
 XX PR 17-JUL-1997; 97US-0052829.  
 XX PA (UNMI ) UNIV MICHIGAN.  
 XX PI Nabel GJ;

XX WPI; 1999-132242/11.  
 DR N-PSDB; AAX21573.  
 XX Method for inhibiting proliferation of a cell - comprises  
 PT administration of FasL protein to the cell locus  
 XX Disclosure; Fig 6A-C; 70pp; English.  
 CC The invention relates to a method for inhibiting the proliferation of a  
 CC suitable cell or pathogen which comprises administering to the cells  
 CC locus an effective amount of FasL. A method for identifying agents which  
 CC modulate FasL stimulation of a localised proinflammatory response is also  
 CC provided. The methods can be used for provoking a proinflammatory  
 CC response in the locus of a cell. It can also be used to inhibit the  
 CC proliferation of a cell or a pathogen in a subject. The present sequence  
 CC represents a rat FasL protein.  
 XX SQ Sequence 278 AA;

Query Match 8.2%; Score 102; DB 20; Length 278;  
 Best Local Similarity 21.7%; Pred. No. 0.038;  
 Matches 52; Conservative 37; Mismatches 105; Indels 46; Gaps 9;  
 QY 14 PSPDPAMQVPGSVASPRSTRPWRSTRSRFYSLTALVCLVAVAILL----VLVVQK 69  
 Db 47 pppppspplppspqppplpplspkdkndielwlpviffmvalvgmglmyqlfhqk 106  
 QY 70 KDSPTNTEKAPLKGNCSEDLFCTLKSTPSK----KSWAYLQVSKHLNNTKLSWNED-G 124  
 Db 107 elaelrefthslrvssfekqi--anpstsetkkprsvahltgnprsrslplewedyg 164  
 QY 125 T--IHGLIYQDGNLIVQPGLYFIVCQLQFLVQCSN-----HSV-----DLTLQLL 168  
 Db 165 talisgvykkgglvineaglyfvyksvfyrgqscnspqshkvymrnfkypgdvlm-- 222  
 QY 169 INSKIKKQTLVTVCESGVQSKNIYQNLSQLFLHYLQVNSTISVRVDNFQYVDNTFPPLDN 228  
 Db 223 -----eeklnycttg-----qiwahssylgavfultvadhlyvnisqlslin 265

RESULT 14  
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 ID AAR79068 standard; Protein; 138 AA.  
 XX AC AAR79068;  
 XX DT 22-FEB-1996 (first entry)  
 XX DE Mouse Fas ligand (partial sequence).  
 XX KW Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;  
 XX KW Fas cell surface antigen; Fas-L; mouse.  
 XX OS Mus musculus.  
 XX PN WO9513293-A1.  
 XX PD 18-MAY-1995.  
 XX PF 10-NOV-1994; 94WO-JP01899.  
 XX PR 18-OCT-1994; 94JP-0278378.  
 XX PR 10-NOV-1993; 93JP-0305975.  
 XX PR 13-DEC-1993; 93JP-0342526.  
 XX PR 18-MAR-1994; 94JP-0074344.  
 XX PR 08-JUL-1994; 94JP-0180955.  
 XX PR 07-SEP-1994; 94JP-0239363.  
 XX PA (MOCH ) MOCHIDA PHARM CO LTD.  
 XX PA (OSAB-) OSAKA BIOSCIENCE INST.  
 XX

```

CC AB0265-83 represent tumour necrosis factor (TNF) ligands. The
CC specification describes an AGP-3 polypeptide, which is TNF ligand
CC family member. AGP-3 is a type II transmembrane protein, and is a
CC potent B cell stimulatory factor. Expression of AGP-3 correlates to
CC increases in the number of B cells and immunoglobulins produced.
CC AGP-3 proteins, antibodies, and nucleic acids may be used to treat
CC inflammatory and immune disorders, e.g. rheumatoid arthritis,
CC Crohn's disease, lupus and graft versus host disease. The nucleic
CC acids may be used to regulate the expression of an AGP-3 related
CC protein. The AGP-3 proteins, antibodies and nucleic acids are also
CC useful for the detection of AGP-3 agonists, antagonists and
CC characterizing interactions with AGP-3 related proteins.
CC
XX
SQ Sequence 143 AA;

Query Match 7.8%; Score 97; DB 21; Length 143;
Best Local Similarity 24.2%; Pred. No. 0.048;
Matches 32; Conservative 28; Mismatches 46; Indels 26; Gaps 6;

QY 102 KSAWLYQVSHLNTKLSWNED-GT--IHGLIYDGNLIQVPGLYFTVCOQLVQ-CS 157
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 6 rsvahlngnphsrslpewedytgalsgvykkgglvinetgylfyvskvyfgrscn 65
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 158 NHSVDLTQLQLINSK-----IKKQTLVTVCESG-----VQSKNIYQNLS 196
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 66 nqpinhkvymr-nskytpedlvlmeekrlnycttggiwahssylgavfnaltsadhlyvnls 124
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QY 197 QFLHLYLQVNST 208
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Db 125 qlslinfeeskT 136
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```

Search completed: September 5, 2001, 10:22:39  
Job time: 54 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 5, 2001, 21:46:06 ; Search time 1370.5 Seconds  
(without alignments)  
4572.960 Million cell updates/sec

Title: US-09-628-126-18  
Perfect score: 663  
Sequence: 1 ATGCAGGTGACGCCGCTC.....TATATAGTAGCTCAGACTGA 663

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues  
Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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7: gb\_est7:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	402.6	60.7	910	106	AL583443	AL583443 AL583443
2	398.2	60.1	670	249	AZ786450	AZ786450 2M0032A02
3	371.6	56.0	634	173	BG092633	BG092633 mac14f02.
4	331.8	50.0	487	170	BF890112	BF890112 289772 MA
5	194.8	29.4	318	144	BF082784	BF082784 PM1-BT075
6	193.2	29.1	463	173	BG091233	BG091233 mac14f02.
7	184.2	27.8	276	118	AW602310	AW602310 RC5-BT055
8	171.6	25.9	277	163	BE073509	BE073509 RC5-BT055
9	131.8	19.9	550	119	AW654920	AW654920 105425 MA
10	122	18.4	552	248	AZ7111040	AZ7111040 RPI-24-1
11	56.4	8.5	219	190	W21054	W21054 zb53el2.r1
12	56.4	8.5	524	24	A1734260	A1734260 zb53el2.y
13	43.6	6.6	284	30	AV520400	AV520400 AV520400
14	40.4	6.1	271	191	Z17941	Z17941 ATTS0425 St
15	40.4	6.1	277	31	AV560475	AV560475 AV560475
16	40.4	6.1	292	30	AV521294	AV521294 AV521294
17	40.4	6.1	332	30	AV521444	AV521444 AV521444
18	40.4	6.1	355	31	AV567141	AV567141 AV567141
19	40.4	6.1	374	30	AV521744	AV521744 AV521744
20	40.4	6.1	386	30	AV520039	AV520039 AV520039
21	40.4	6.1	389	31	AV564529	AV564529 AV564529
22	40.4	6.1	402	31	AV559152	AV559152 AV559152
23	40.4	6.1	403	31	AV535696	AV535696 AV535696
24	40.4	6.1	403	31	AV562974	AV562974 AV562974
25	40.4	6.1	404	31	AV557417	AV557417 AV557417
26	40.4	6.1	405	30	AV520434	AV520434 AV520434
27	40.4	6.1	413	31	AV532827	AV532827 AV532827
28	40.4	6.1	418	30	AV521190	AV521190 AV521190
29	40.4	6.1	456	31	AV532155	AV532155 AV532155
30	40.4	6.1	459	31	AV565123	AV565123 AV565123
31	40.4	6.1	469	31	AV563334	AV563334 AV563334
32	40.4	6.1	470	30	AV564610	AV564610 AV564610
33	40.4	6.1	474	30	AV521394	AV521394 AV521394
34	40.4	6.1	484	31	AV532167	AV532167 AV532167
35	40.4	6.1	491	31	AV558040	AV558040 AV558040
36	40.4	6.1	495	6	AA394710	AA394710 26493 Lam
37	40.4	6.1	499	104	AI996279	AI996279 701550991
38	40.4	6.1	500	31	AV567354	AV567354 AV567354
39	40.4	6.1	502	31	AV555752	AV555752 AV555752
40	40.4	6.1	508	31	AV558545	AV558545 AV558545
41	40.4	6.1	519	31	AV522496	AV522496 AV522496
42	40.4	6.1	521	30	AV520869	AV520869 AV520869
43	40.4	6.1	527	31	AV555876	AV555876 AV555876
44	40.4	6.1	538	31	AV557470	AV557470 AV557470
45	40.4	6.1	543	31	AV564710	AV564710 AV564710

ALIGNMENTS

RESULT	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1	AL583443	AL583443 LTI_NFL010_BC2 Homo sapiens cDNA clone CS0DL012YA12 5 prime, mRNA sequence.	AL583443	AL583443.1	GI:12952410	EST.	human.	1 (bases 1 to 910)	Li W.B., Gruber C., Jessee J. and Polayes D.	Full-length cDNA libraries and normalization	Unpublished (2001)	Contact: Genoscope

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 1 (bases 1 to 910)  
 Li W.B., Gruber C., Jessee J. and Polayes D.  
 Full-length cDNA libraries and normalization  
 Unpublished (2001)  
 Contact: Genoscope

Genoscope - Centre National de Sequencage  
 BP 191 91006 EVRY cedex - France  
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
 Location/Qualifiers  
 1. 910  
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 /clone="CS0DL012YA12"  
 /clone\_lib="LTI\_NFL010\_BC2"  
 /sex="male"  
 /tissue\_type="B cells from Burkitt lymphoma"  
 /note="Vector: pCMVSPORT 6; Site 1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371  
 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"

BASE COUNT 244 a 232 c 204 g 225 t 5 others  
 ORIGIN  
 Query Match 60.7%; Score 402.6; DB 106; Length 910;  
 Best Local Similarity 78.7%; Pred. No. 3.3e-112;  
 Matches 490; Conservative 3; Mismatches 127; Indels 3; Gaps 1;  
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 QY 101 TGTGCTTTGTGTGGCAGTGGGATCTTCTGCTAGTCCAGAAAAGAGACTCCA 160  
 Db 330 TGTGCTTTGTGTGGCAGTGGGATCTTCTGCTAGTCCAGAAAAGAGACTCCA 389  
 QY 161 CTCCAAATACAACTGAG 220  
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 QY 221 GTACCTGAAAGTACTCCTCAGCAAGTCCCTCCCTCCTCCTCCTCCTCCTCCTCCT 280  
 Db 450 GTATCTGAAAGTACTCCTCAGCAAGTCCCTCCCTCCTCCTCCTCCTCCTCCTCCT 509  
 QY 281 TCAACAATACCAAACTGTCATGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 340  
 Db 510 TAAACAACAAGTGTCTTGGAAACAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 569  
 QY 341 ACGGGAACCTGATAGTCCAAATCCCTGGCTGTGTACTTTCATCGTTTGGCAACTGCAGTTCC 400  
 Db 570 ATGGGAATCTGTGTATCCAAATCCCTGGCTGTGTACTTTCATCGTTTGGCAACTGCAGTTTC 629  
 QY 401 TCGTGCAGTCTCAATCATCTTCTGGACCTCAGATTCAGCTCCTCATCAATTCACA 460  
 Db 630 TTGTACAATGCCAAATTAATTTCTGCGATCTGAAGTCTGAGCTTCTCATCAACAAGCATA 689  
 QY 461 TCAAAAAGCAGACGTTGTGTACAGTGTGTGAGTCTGGAGTTCAGAGTGAAGAATCTACC 520  
 Db 690 TCAAAAAGCAGACGTTGTGTACAGTGTGTGAGTCTGGAGTTCAGAGTGAAGAATCTACC 749  
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 Db 750 AGAATCTCTCAGTTTTTGTGCTGCAATTTACTTACAGGTCAACTCTTACCATATACAGTTCAGGG 809  
 QY 581 TGGATAATTCAGTATGATGATCAACAACACTTCCCTCTCTGTGATGATGCTATCCGCTCT 640  
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 QY 641 TCTATATAGTAGCTCAGACTGA 663  
 Db 870 TCTATACAGTAATTCAGACTGA 892

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ORIGIN
Query Match      56.0%; Score 371.6; DB 173; Length 634;
Best Local Similarity 92.0%; Pred. No. 9.2e-103;
Matches 392; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 82 CTCAGACACCGCACTGGTGTGCTTGTGGTGGAGTGGCGATCATCTGGTACTGGTA 141
DB 634 CTAAGAACCCCGCAGTGGGTGCTTGTGGTGGCAGTGAGAATCATCTCTGGTCTGGTA 575
QY 142 GTCAGAGAAAGACTCCACTCCAAATACAACTGAGAAGGCCCCCTTAAAGGAGGAAT 201
DB 574 GTCCAGACTATGGATCCACTCCAAATACAACTGAGAAGGCCCCCTTAAAGGAGGAAT 515
QY 202 TGCTCAGAGGATCTCTCTGTCACCTCGAAAGTACTCCATCCAAAGTATGATGGCTAC 261
DB 514 TGCTCAGAGGTTCTCTCTGTCACCTCGAAAGTACTCCATCCAAAGTATGATGGCTAC 455
QY 262 CTCCAAGTCTCAAGCATCTCAACATATACAACTGTCTGGAACGAAGATGGCACCATC 321
DB 454 CTCCAAGTCTCTAGCATCTCAACATATACAACTGTCTGGAACGAAGATGGCACCATC 395
QY 322 CACGGACTCATATACAGAGCGGAACCTGATAGTCCAAATCATCTGTCGCTGTGTTTTCATC 381
DB 394 CACGGACTCATATACAGAGCGGAACCTGATAGTCCAAATCATCTGTCGCTGTGTTTTCATC 335
QY 382 GTTTCGCAACTGCAGTTCCTCTGTCAGTGTCTCAATCATCTGTCGACCTGACATTCGAG 441
DB 334 GTTTCGCAACTGCAGTTCCTCTGTCAGTGTCTCAATCATCTGTCGACCTGACATTCGAG 275
QY 442 CTCCTCATCAATTCCAAGTCAAAAAGCAGACGCTTGGTACAGTGTGTGAGTCTGGAGTT 501
DB 274 CTCCTCATCAATTCCAAGTCAAAAAGCAGACGCTTGGTACAGTGTGTGAGTCTGGAGTT 215
QY 502 CAGAGT 507
DB 214 CAGAGT 209

RESULT 4
BF890112 487 bp mRNA EST 18-JAN-2001
LOCUS 289772 MARC 3BOV Bos taurus cdna 5', mRNA sequence.
ACCESSION BF890112
VERSION BF890112.1 GI:12281570
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 487)
AUTHORS Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M.,
Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid
,W.W. and Keele,J.W.
Design and use of four pooled tissue normalized cdna libraries for
EST discovery in cattle
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCGAGTCAGCAGC
Plate: 96 row N column: 9
Seq primer: ATTTAGGTGACACTATAG.

FEATURES
source
Location/Qualifiers
1..487
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="vector: pcMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendinosus muscle, and fetal
longissimus muscle."
BASE COUNT 148 a 125 c 106 g 108 t
ORIGIN

Query Match      50.0%; Score 331.8; DB 170; Length 487;
Best Local Similarity 80.1%; Pred. No. 1.3e-90;
Matches 390; Conservative 0; Mismatches 97; Indels 0; Gaps 0;

QY 124 ATCATCTCTGGTACTGGTACTCCAGAAAAGGACTCCACTCCAAATACAACTGAGAAGGCC 183
DB 1 ACCATTATGTGCTGTGGTACTCCAGAAAGGAGTCCATTCCCAACCCCGCGGCAATTC 60
QY 184 CCCCTTAAAGGAGCAAAATTTGCTCAGAGGATCTCTCTGTCACCTGAAAAGTACTCCATCC 243
DB 61 CCCCTTAAAGGAGGGAATTTGCTCAGAGGACATCTCATGTATCTCTGAAAAGGCTCCATTC 120
QY 244 AAGAAGTCATGGGCTTACTCTCAAGTGTCAAGGATCTCAACAATATACCAAACTGTCTATGG 303
DB 121 AAGAAATCATGGGCTTACTCTCAAGTGTCAAGGATATATAACAACCAACCCAGTTGTCTTGG 180
QY 304 AACGAAGATGGCACTCCAGGACTCATATACAGAGCGGGAACCTGATAGTCCAATTC 363
DB 181 AACAAAGATGCATCATCCATGGAGTCAGATATCAGGATGAGAACCTGGTGTATCCAGTTC 240
QY 364 CCTGGCTGTACTTCATCTGTTGCCAACTGCTCCAGTTCCTCTGTCAGTGTCTCAAAATCATCT 423
DB 241 CCAGGTGGTACTTCATCATCTGCCAACTGCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 300
QY 424 GTGGACCTGACATTCGACGCTCTCATCAATTCCAAGATCAAAAAGCAGACGCTGTGTACACA 483
DB 301 GTCACCTGAGCTGGAGCTCTCATCAACAAGAGCTTAAAGAGCAGACCTGGTGACA 360
QY 484 GTGTGTGAGTCTGGAGTTCAGAGTAAGAATCATCTACCAAGATCTCTCTCAAGTCTTTTGTG 543
DB 361 GTGTGTGAGTCTGGAGCACAAACCAAGAACATATACCAAGAACCTCTCCAGTCTTCTTGTG 420
QY 544 CATTACTACAGGTCAACTCTACCATATACAGTCCAGGTGGGATATTTCCAGTATGTGGAT 603
DB 421 GAACACCTCCAGGTCAACACCACCATATCATGTCAGGTGGGATATTTCCAGTATGTGGAT 480
QY 604 ACAAACA 610
DB 481 ACAAACA 487

RESULT 5
BF082784 318 bp mRNA EST 18-OCT-2000
LOCUS PM1-BT0759-050900-007-e04 BT0759 Homo sapiens cdna, mRNA sequence.
DEFINITION BF082784
ACCESSION BF082784
VERSION BF082784.1 GI:10876614
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 318)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Brienes,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
,.,.,.
```



.M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
PROC. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-RC5-BT0559-140>)  
200-012-E03&t3-2000-02-14&t4-1)  
Seq primer: puc 18 forward  
High quality sequence stop: 277.

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this sequence was derived from the FAREs7/hick human cancer genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-RC5-BP0559-140
200-012-E03at3-2000-02-14&wt4=1)
Seq primer: puc 18 forward
High quality sequence stop: 277.
Location/Qualifiers
1. 277
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="BP0559"
/dev_stage="Adult"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTS PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT      80 a      63 c      56 g      78 t

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```
mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT      80 a       63 c     56 g       78 t
ORIGIN
Query Match          25.9%; Score 171.6; DB 163; Length 277;
Best Local Similarity 79.6%; Pred. No. 1.3e-41;
Matches 215; Conservative 0; Mismatches 54; Indels 1; Gaps 1;
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QY	327	ACTCATATACCAGACGGGAACTGTAGTCCAATTCCCTGGCTTGTA	CTTCACTTCATCGTTG	386
Db	1	AGTCAGATATCAGATGGGAATCTGGTGATTCAAATCCCTGGTTGT	TACTTTCATCATTTG	60
QY	387	C-CAACTGCAGTTCCCTCGTGCAGTGTCAAATCAATCTGTGTG	GACCTGACATTCGAGCTCC	445
Db	61	CGAACCTGCGAGTTCTTGTAACAATGCCAATAAATCTGTCG	ATCTTGAAGTTGGAGCTTC	120
QY	446	TCATCAATTCCAAGATCAAAAAGCAGACGTTGGTGAACAGTG	TGTGAGTCTCGAGTTCAGA	505
Db	121	TCATCACAGCGATATCAAAAAACAGGCCCTGGTGACAGTGT	GAGTCTGGAATGCANA	180
QY	506	GTAAGAACATCTACCGAATCTCTCTCAGTTTTTGTCTGCA	FATTACAGTCAACTCTA	565
Db	181	CGAAACACGATACCGAATCTCTCTCAATTTCTTGCTGG	AATTACCTGCAGGTCAACACCA	240
QY	566	CCATATCAGTCAGGTGGATAAATTTCCAGT		595
Db	241	CCATATCAGTCAATGTGGATACATTCAGT		270

QY	566	CCATATCAGTCAGGGTGGATAAATTTCAGT	595
Db	241	CCATATCAGTCAATGTGGATACATTCCAGT	270
RESULT	9		
AW654920		550 bp	mRNA
LOCUS	AW654920		EST
DEFINITION	105435 MARC 1BOV Bos taurus CDNA 5', mRNA sequence.		14-JUL-2000
ACCESSION	AW654920		
VERSION	AW654920.1		
KEYWORDS	EST.		
SOURCE	cow.		
ORGANISM	Bos taurus		
	Eukaryota;		
	Mammalia;		
	Eutheria;		
	Cetartiodactyla;		
	Ruminantia;		
	Pecora;		
	Bovoides;		
	Vertebrata;		
	Euteleostomi;		

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Bovidae; Bovinae; Bos.  
1 (bases 1 to 550)  
Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M.,  
Bennett, G.A., Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Laegreid,  
W.W., and Keele, J.W.  
Design and use of four pooled tissue normalized cDNA libraries for  
EST discovery in cattle  
Unpublished (2000)  
Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smithem@mail.marc.usda.gov  
Single pass sequencing. Bases called and alt trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 18  
and -minmatch 12 options.  
PCR Primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCACGTCACGACG  
Plate: 82 row: B column: 22  
Seq primer: ATTAGGTGACACTATAG.

FEATURES  
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Location/Qualifiers  
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/organism="Bos taurus"  
/db\_xref="taxon:9913"  
/clone\_lib="MARC 1BOV"  
/tissue\_type="pooled"  
/lab\_host="DH10B"  
/note="vector: pCMV SPORT6; Site\_1: XbaI; Site\_2: XhoI;  
Library made from pooled tissue from lymph node, ovary,  
fat, hypothalamus, and pituitary."  
124 a 162 c 153 g 111 t

BASE COUNT  
ORIGIN

Query Match 19.9%; Score 131.8; DB 119; Length 550;  
Best Local Similarity .76.2%; Pred. No. 2.7e-29;  
Matches 176; Conservative 0; Mismatches 52; Indels 3; Gaps 1;

QY 42 CACGAGCCCTGGGACACACACAAAGTCGAGCTACTCTACCTCAGCAGCACCCGCTGG- 100  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 320 CACCAGCCACTGGGGAACACCGGGCGGGGACTCTGCTTACCCAGCCGCTCGCTGGC 379  
QY 101 --TGTGCTTGTGTGGCAGTCGGCATCTGCTGTACTGGTAGTCCAGAAAAGGACTC 158  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 380 TCTGTGCTGCTGTTGCTGTGGCCAGCATTTATGCTGTGGTAGTTCAGAGAGCGACTC 439  
QY 159 CACTCCAAATCACTAGAGAGGCCGCCCTTTAAAGAGGAGAAATGCTCAGAGGATCTCTT 218  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 440 CATTCCCAACCGCGGGGCAATTCCTTAAAGGAGGGAATGCTCAGAGGACATCTC 499  
QY 219 CTGTACCTGAAAGTACTCTCCATCAAGAGTCATGGGCTACCTCCAAGT 269  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 500 ATGTCTCTGAAAGGGCTCCATTCAGAAATCATGGGCTACCTCCAAGT 550

RESULT 10  
AZ711040  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

AZ711040 552 bp DNA GSS 24-JAN-2001  
RPCI-24-132J17.TVC RPCI-24 Mus musculus genomic clone  
RPCI-24-132J17, DNA sequence.  
A2711040  
A2711040.1 GI:12443209  
GSS.  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 552)  
Zhao, S., Nieman, W., Malek, J., Shatsman, S., Akinret, B., Levins, M.,  
Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregorgis, E.,  
Russell, D., de Jong, P. and Fraser, C.M.

TITLE  
JOURNAL  
COMMENT

Mouse BAC End Sequences from Library RPCI-24  
Unpublished (1999)  
Other GSSs: RPCI-24-132J17.TJ  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the mouse BAC library RPCI-24. For BAC  
library availability, please contact Pieter de Jong  
Resources (http://www.tigr.org/bacpac/orderingframe.htm). BAC end  
plate: http://www.tigr.org/tldb/bac\_ends/mouse/bac\_end\_intro.html  
Plate: 132 row: J column: 17  
Seq primer: T7  
Class: BAC ends.

FEATURES  
Source  
Location/Qualifiers  
1..552  
/organism="Mus musculus"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="RPCI-24-132J17"  
/clone\_lib="RPCI-24"  
/sex="Male"  
/cell\_type="Spleen/Brain"  
/note="vector: pTARBAC1; Site\_1: BamHI; Site\_2: BamHI;  
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The  
library was cloned in the pTARBAC1 cloning vector at the  
BamHI sites using MboI partially digested male C57BL/6J  
DNA."  
166 a 118 c 111 g 157 t

BASE COUNT  
ORIGIN

Query Match 18.4%; Score 122; DB 248; Length 552;  
Best Local Similarity 100.0%; Pred. No. 2.7e-26;  
Matches 122; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 542 TGCATTACTACAGTCAACTCTACCATATCAGTCAGGTCGGTGAATTTCCAGTATGG 601  
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Db 1 TGCATTACTACAGTCAACTCTACCATATCAGTCAGGTCGGTGAATTTCCAGTATGG 60  
QY 602 ATACAAACACTTTCCCTCTTGATAATGCTATCGCTCTTCTTATATAGTACGTCAGACT 661  
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 61 ATACAAACACTTTCCCTCTTGATAATGCTATCGCTCTTCTTATATAGTACGTCAGACT 120  
QY 662 GA 663  
Db 121 GA 122

RESULT 11  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS

W21054 219 bp mRNA EST 20-AUG-1996  
2b53e12.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone  
IMAGE:307342 5' similar to gb:L09753 CD30 LIGAND (HUMAN);, mRNA  
sequence.  
W21054  
W21054.1 GI:1297930  
EST.  
human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
1 (bases 1 to 219)  
Hillier, L., Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B.,  
Chissoe, S., Dietrich, N., Dubuque, T., Favello, A., Gish, W., Hawkins,  
M., Hultman, M., Kucaba, T., Lacy, M., Le, N., Mardis, E., Moore,  
B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T.,  
Schellenberg, K., Soares, M.B., Tan, F., Thierfry-Meg, J., Trevisakis, E.,  
Underwood, K., Wohlmann, P., Waterston, R., Willson, R. and Marra, M.

Email: [cqapps-r@mail.nih.gov](mailto:cqapps-r@mail.nih.gov)

Location/Qualifiers

Location/Qualifiers

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source
1..284
/organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="AP219a08F"
/clone_lib="Arabidopsis thaliana aboveground organs two to
six-week old"
/tissue_type="aboveground organs"
/dev_stage="two to six-week old"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT      79 a   66 c   72 g   67 t
ORIGIN

Query Match      6.6%; Score 43.6; DB 30; Length 284;
Best Local Similarity 55.2%; Pred. No. 0.022;
Matches 85; Conservative 0; Mismatches 69; Indels 0; Gaps 0;

QY 431 TGACATTGCAGCTCCTCATCAATTCGAAGATCAAAAAGCAGAGCTGGTAACAGTGTG 490
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 96 TCATCAAGCAGGTTCTGTAAAGTCCACACCGTCACTAGTCTCTGGATAAAGTAACCG 155

QY 491 AGTCTGGAGTTCAGATAGACATACACAGATCTCTCAGTTTCTGCTGCACTACT 550
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Db 156 AGGATGGCGAGCATAGCCAGTCTATCGTTCTTGACCTCTTGAGTTTCAGCTCCTTCAGT 215

QY 551 TACAGGTCACACTACCATATCAGTCAGGTGGA 584
      || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 216 GACTTCTCATCTTTCCCAACCAAGAGGGTTGA 249

RESULT 14
Z17941/c Z17941 271 bp mRNA EST 10-NOV-1992
LOCUS ATTS0425 Strasbourg-A Arabidopsis thaliana cDNA clone SASFB04 5'
DEFINITION similar to Tomato type III chlorophyll a/b binding polypeptide of
photocystem I (Cab-8). GenBank entry X15258, mRNA sequence.
ACCESSION Z17941
VERSION Z17941.1 GI:17069
KEYWORDS EST, thale cress.
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 271)
AUTHORS CNRS.
TITLES The Arabidopsis thaliana transcribed genome: the GDR cDNA program
JOURNAL Unpublished (1996)
COMMENT Contact: Parmentier Y., Criqui M.C., Durr A., Fleck J.
Fleck Jacqueline / 1626
Biologie Moleculaire des Plantes - CNRS
12 Rue du General Zimmer, 67084 Strasbourg Cedex, France
Email: ARABANK@MEDOC.U-STRASBG.FR.
FEATURES
source
1..271
/organism="Arabidopsis thaliana"
/strain="ecotype Columbia"
/db_xref="taxon:3702"
/clone="SASFB04"
/clone_lib="Strasbourg-A"
/note="Vector: Lambda ZAPII; tissue-sliced leaves of
A.thaliana ecotype Columbia; clone_library=Strasbourg-A;
Cloning vector: Lambda ZAPII; Physiological condition:
leaves strips incubated 2/3/4 days in liquid culture
medium."
BASE COUNT      67 a   65 c   72 g   67 t
ORIGIN

Query Match      6.1%; Score 40.4; DB 191; Length 271;
Best Local Similarity 53.9%; Pred. No. 0.21;

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Matches 83; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 431 TGACATTGCAGCTCCTCATCAATTCGAAGATCAAAAAGCAGAGCTGGTAACAGTGTG 490
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 228 TGATCAAGCAGGTTCTGTAAAGTCCACACCGTCACTAGTCTCTGGATAAAGTAACCG 169

QY 491 AGTCTGGAGTTCAGATAGACATCTACCAAGATCTCTCAGTTTCTGCTGCACTACT 550
      || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 168 AGGATGGCGAGCATAGCCAGTCTATCGTTCTTGACCTCTTGAGTTTCAGCTCCTTCAGT 109

QY 551 TACAGGTCACACTACCATATCAGTCAGGTGGA 584
      || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 108 GACTTCTCATCTTTCCCAACCAAGAGGGTTGA 75

RESULT 15
AV560475 277 bp mRNA EST 07-SEP-2000
LOCUS AV560475 Arabidopsis thaliana green siliques Columbia Arabidopsis
DEFINITION thaliana cDNA clone SQ135c06F 3', mRNA sequence.
ACCESSION AV560475
VERSION AV560475.1 GI:8731901
KEYWORDS EST, thale cress.
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana
REFERENCE 1 (bases 1 to 277)
AUTHORS Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
TITLES Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
JOURNAL 1 (bases 1 to 277)
MEDLINE DNA Res. 7, 175-180 (2000)
COMMENT Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizukazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
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/strain="Columbia"
/db_xref="taxon:3702"
/clone="SQ135c06F"
/clone_lib="Arabidopsis thaliana green siliques Columbia"
/tissue_type="green siliques"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT      66 a   79 c   63 g   69 t
ORIGIN

Query Match      6.1%; Score 40.4; DB 31; Length 277;
Best Local Similarity 53.9%; Pred. No. 0.21;
Matches 83; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 431 TGACATTGCAGCTCCTCATCAATTCGAAGATCAAAAAGCAGAGCTGGTAACAGTGTG 490
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 2 TGATCAAGCAGGTTCTGTAAAGTCCACACCGTCACTAGTCTCTGGATAAAGTAACCG 61

QY 491 AGTCTGGAGTTCAGATAGACATCTACCAAGATCTCTCAGTTTCTGCTGCACTACT 550
      || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 62 AGGATGGCGAGCATAGCCAGTCTATCGTTCTTGACCTCTTGAGTTTCAGCTCCTTCAGT 121

QY 551 TACAGGTCACACTACCATATCAGTCAGGTGGA 584
      || ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 122 GACTTCTCATCTTTCCCAACCAAGAGGGTTGA 155

Search completed: September 6, 2001, 00:14:53

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 5, 2001, 21:55:46 ; Search time 68.95 Seconds  
(without alignments)  
1820.352 Million cell updates/sec

Title: US-09-628-126-18  
Perfect score: 663  
Sequence: 1 ATCAGGTGACGCCGCTC.....TATATAGTACTGACTGCA 663

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 324599 seqs, 94655562 residues

Total number of hits satisfying chosen parameters: 649198

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
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5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	663	100.0	663	1	US-08-225-989-18
2	663	100.0	663	1	US-08-570-923-18
3	663	100.0	663	1	US-08-580-014-18
4	663	100.0	663	3	US-09-079-785-18
5	663	100.0	720	1	US-08-225-989-5
6	663	100.0	720	1	US-08-570-923-5
7	663	100.0	720	1	US-08-580-014-5
8	663	100.0	720	3	US-09-079-785-5
9	402.2	60.7	648	1	US-08-225-989-22
10	402.2	60.7	648	1	US-08-570-923-22
11	402.2	60.7	648	1	US-08-580-014-22
12	402.2	60.7	648	3	US-09-079-785-22
13	402.2	60.7	705	1	US-08-225-989-7
14	402.2	60.7	705	1	US-08-570-923-7
15	402.2	60.7	705	1	US-08-580-014-7
16	402.2	60.7	705	3	US-09-079-785-7
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18	33.2	5.0	1501	2	US-08-145-6580-24
19	32	4.8	1526	1	US-08-694-915-3
20	31	4.7	180	6	5508199-1
21	31	4.7	1566	2	US-08-145-6580-13
22	31	4.7	1566	2	US-08-145-6580-22
23	31	4.7	1568	2	US-08-145-6580-20
24	31	4.7	1571	2	US-08-145-6580-21
c 25	30.8	4.6	2793	1	US-08-209-747-1
c 26	30.8	4.6	2793	1	US-08-458-298-1
27	30.6	4.6	1720	3	US-08-705-771-2

28	30.4	4.6	720	4	US-08-913-014A-4	Sequence 4, Appli
29	30.4	4.6	1353	4	US-08-913-014A-6	Sequence 6, Appli
30	30.4	4.6	1491	4	US-08-913-014A-5	Sequence 5, Appli
31	30.2	4.5	1480	3	US-09-090-793-4	Sequence 4, Appli
c 32	29.6	4.5	87350	3	US-08-781-891-79	Sequence 79, Appli
33	29.4	4.4	1569	2	US-08-145-6580-23	Sequence 23, Appli
34	29.2	4.4	940	4	US-09-479-524-2	Sequence 2, Appli
c 35	29.2	4.4	940	4	US-09-479-524-8	Sequence 8, Appli
36	29.2	4.4	1171	5	PCT-US95-00362-4	Sequence 4, Appli
c 37	29.2	4.4	2215	3	US-08-891-789B-7	Sequence 7, Appli
c 38	29	4.4	1569	1	US-08-368-260-1	Sequence 1, Appli
c 39	29	4.4	1569	2	US-08-559-221-1	Sequence 1, Appli
c 40	29	4.4	1635	3	US-09-234-332-4	Sequence 4, Appli
c 41	29	4.4	2214	3	US-08-864-038A-1	Sequence 1, Appli
c 42	29	4.4	3114	3	US-08-946-026-12	Sequence 12, Appli
c 43	29	4.4	3331	3	US-08-864-038A-2	Sequence 2, Appli
c 44	29	4.4	3331	3	US-08-864-038A-4	Sequence 4, Appli
c 45	29	4.4	68750	3	US-09-335-409-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1  
US-08-225-989-18  
; Sequence 18, Application US/082255989  
; Patent No. 5480981  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644



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; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 663 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: mucD30-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..663
;
US-08-225-989-18

Query Match      100.0%; Score 663; DB 1; Length 663;
Best Local Similarity 100.0%; Pred. No. 2.4e-209;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 ATGCAGGTGCAGCCCGCTCGGTAGCCAGCCCTGGAGAGACGACGAGCCCTGGAGAAGC 60
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DB 61 ACAAGTCCAGCTACTTCTACCTCAGCACCACCGCACTGGTGTGCTTGTGGCAGTG 120
QY 121 CGGATCATTTCTGGTACTGCTCAGCAAGAAAGGACTCCCACTCCAATACAACGTAGAAG 180
DB 121 CGGATCATTTCTGGTACTGCTCAGCAAGAAAGGACTCCCACTCCAATACAACGTAGAAG 180
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DB 181 GCCCCCTTAAAGGAGGAATGCTCAGAGGATCTCTTCTGTACCTCGTAAAGTACTCCA 240
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DB 241 TCCAGAGAGTGCATGGCCCTACTCTCAAGTGTCAAGAGCATCTCAACAATACCAACGTCA 300
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QY 661 TGA 663
DB 661 TGA 663
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US-08-570-923-18

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[illegible]

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RESULT
US-08-580-014-18
; Sequence 18, Application US/08580014
; Patent No. 5753203
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580.014

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FILING DATE: 20-DEC-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION NUMBER: US/08/225,989  
FILING DATE: 12 APRIL 1994  
APPLICATION NUMBER: US 07/966,775  
FILING DATE: 27-OCT-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 663 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: mUCD30-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..663  
US-08-580-014-18

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Query Match      100.0%; Score 663; DB 1; Length 663;
Best Local Similarity 100.0%; Pred. No. 2.4e-209;
Matches 663: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY	181	GCCCCCTTAAAGGAGGAAATTGCTCAGAGAGATCTCTTGTAACCTGAAAAGTACTCCA	240
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QY 661 TGA 663
Db 661 TGA 663

RESULT 4
US-09-079-785-18
; Sequence 18, Application US/09079785
; Patent No. 6143869
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 6143869el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,785
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
```

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; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 663 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: mUCD30-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..663
; US-09-079-785-18

Query Match 100.0%; Score 663; DB 3; Length 663;
Best Local Similarity 100.0%; Pred. No. 2.4e-209;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCAGGTGCAGCCCGCTCGGTAGCCAGCCCTGGAGAGCAGCAGGCGCTGAGAGC 60
Db 1 ATGCAGGTGCAGCCCGCTCGGTAGCCAGCCCTGGAGAGCAGCAGGCGCTGAGAGC 60
QY 61 ACAAGTGCAGCTACTTCTACCTCAGCACCCACCCTGCTGTGCTTGTGTGGCAGTG 120
Db 61 ACAAGTGCAGCTACTTCTACCTCAGCACCCACCCTGCTGTGCTTGTGTGGCAGTG 120
QY 121 GCGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 121 GCGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
QY 181 GCGCCCTTAAAGGAGGAAATGCTCAGAGGATCTCTCTGCTACCTGAAAGTACTCCA 240
Db 181 GCGCCCTTAAAGGAGGAAATGCTCAGAGGATCTCTCTGCTACCTGAAAGTACTCCA 240
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Db 241 TCCAAGAGTCAATGGGCTTACCTCCTCAAGTGTCAAGGATCTCAACAAATACCAACTGTCA 300
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QY 481 ACAGTGTGTGAGTGTGAGTTCAGAGTGAAGAACATCTACAGAAATCTCTCTCAGTTTTGG 540
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QY 661 TGA 663
Db 661 TGA 663
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RESULT 5  
US-08-225-989-5  
; Sequence 5, Application US/08225989  
; Patent No. 5480981  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: NO. 5480981el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 5:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 720 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; IMMEDIATE SOURCE:  
; CLONE: muCD30-L  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..720  
; US-08-225-989-5

Query Match 100.08; Score 663; DB 1; Length 720;  
Best Local Similarity 100.08; Pred. No. 2.5e-209;  
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCAGGTGCGAGCCCGCTCGGTAGCCAGCCCTGGAGAAGCAGGAGCCCTGGAGAAGC 60  
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Db 58 ATGCAGGTGCGAGCCCGCTCGGTAGCCAGCCCTGGAGAAGCAGGAGCCCTGGAGAAGC 117  
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Db 118 ACAAGTGCAGCTACTTCTACCTCAGCAGCACCACCGCAGCTGGTGTGCTTGTGTGGCAGTG 177  
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Db 178 GCGATCATTCGTGCTAGTGTAGTCCAGAAAAGGAGCTCCATCCAAAATACAACTGAGAAG 237  
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Db 238 GCGCCCTTAAAGGAGGAAATTTGCTCAGAGGATCTCTTCTACCTGAAAAGTACTCCA 297  
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QY 661 TGA 663  
|||  
Db 718 TGA 720  
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RESULT 6  
US-08-570-923-5  
; Sequence 5, Application US/08570923  
; Patent No. 5677430  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570.923
; FILING DATE: 12-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225.989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966.775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 720 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: mucD30-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..720
; US-08-570-923-5

Query Match 100.0%; Score 663; DB 1; Length 720;
Best Local Similarity 100.0%; Pred. No. 2.5e-209;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGACAGTGCAGCCGGCTCGGTAGCCAGCCCTGGAGAACGACGAGGCCCTGGAGAACG 60
Db 58 ATGACAGTGCAGCCGGCTCGGTAGCCAGCCCTGGAGAACGACGAGGCCCTGGAGAACG 117
QY 61 ACAAGTGCAGCTACTTCTACTCTAGCAGCCAGCCGCTGCTGCTGCTGCTGCTGCTG 120
Db 118 ACAAGTGCAGCTACTTCTACTCTAGCAGCCAGCCGCTGCTGCTGCTGCTGCTGCTG 177
QY 121 CGCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 180
Db 178 CGCATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 237
QY 181 GCCCCCCCTTAAGGAGGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
Db 238 GCCCCCCCTTAAGGAGGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 297
QY 241 TCCAGAGTCAATGGGCTTACCTCCAGTGTCAAGCATCTCAAGCATCTCAAGCATCTCA 300
Db 298 TCCAGAGTCAATGGGCTTACCTCCAGTGTCAAGCATCTCAAGCATCTCAAGCATCTCA 357
QY 301 TGGAAACGAAGTGCACCATCCAGGACTCATATACGAGGAGGGAACCTGATAGTCCAA 360

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Db 358 TGGAAACGAAGTGCACCATCCAGGACTCATATACGAGGAGGGAACCTGATAGTCCAA 417
QY 361 TTCCCTGGCTTGTACTTCATCGTTTGGCAACTGCAGTTCTCGTGCGAGTGTCAAATCAT 420
Db 418 TTCCCTGGCTTGTACTTCATCGTTTGGCAACTGCAGTTCTCGTGCGAGTGTCAAATCAT 477
QY 421 TCTGTGGACCTGACATTTGCAGCTCCTCATCAATTCCTCAAGATCAAAAAGCAGACGTTGGTA 480
Db 478 TCTGTGGACCTGACATTTGCAGCTCCTCATCAATTCCTCAAGATCAAAAAGCAGACGTTGGTA 537
QY 481 ACAGTGTGCTGAGTCTGGAGTTTCAGAGTAAGAACAATCTACCAAGATCTCTCTCAGTTTTTG 540
Db 538 ACAGTGTGCTGAGTCTGGAGTTTCAGAGTAAGAACAATCTACCAAGATCTCTCTCAGTTTTTG 597
QY 541 CTGCATTACTTACAGGTCAACTCTTACCATATCAGTCAAGGTGGATAATTTCCAGTATGTG 600
Db 598 CTGCATTACTTACAGGTCAACTCTTACCATATCAGTCAAGGTGGATAATTTCCAGTATGTG 657
QY 601 GATACAAACACTTTCCCTCTTGATAATGTGCTATCCGCTCTTCTTATATAGTAGTCAGAC 660
Db 658 GATACAAACACTTTCCCTCTTGATAATGTGCTATCCGCTCTTCTTATATAGTAGTCAGAC 717
QY 661 TGA 663
Db 718 TGA 720

RESULT 7
US-08-580-014-5
; Sequence 5, Application US/08580014
; Patent No. 5753203
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,014
; FILING DATE: 20-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:

```

NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 720 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: mucD30-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..720  
US-08-580-014-5

Query Match 100.0%; Score 663; DB 1; Length 720;  
Best Local Similarity 100.0%; Pred. No. 2.5e-209; Indels 0; Gaps 0;  
Matches 663; Conservative 0; Mismatches 0;

QY 1 ATGCAGTGCAGCCGGCTCGGTAGCCAGCCCTGGAGAGCAGCAGGCGCTGGAGAAGC 60  
DB 58 ATGCAGTGCAGCCGGCTCGGTAGCCAGCCCTGGAGAGCAGCAGGCGCTGGAGAAGC 117  
QY 61 ACAAGTCGAGCTACTTCTACCTCAGACACACCGCAGCTGTGTGCTTGTGTGGCAGTG 120  
DB 118 ACAAGTCGAGCTACTTCTACCTCAGACACACCGCAGCTGTGTGCTTGTGTGGCAGTG 177  
QY 121 GCGATCATTTCTGTACTGTGTAGTCCAGAAAAGAGCTCCACTCCAATACAACTGAGAAG 180  
DB 178 GCGATCATTTCTGTACTGTGTAGTCCAGAAAAGAGCTCCACTCCAATACAACTGAGAAG 237  
QY 181 GCCCCCTTTAAAGGAGAAATTCCTCAGAGGATCTCTCTGTACCCCTGAAAGTACTCCA 240  
DB 238 GCCCCCTTTAAAGGAGAAATTCCTCAGAGGATCTCTCTGTACCCCTGAAAGTACTCCA 297  
QY 241 TCCAGAAGTCATGGGCGCTACCTCCAAAGTGTCAAAGCATCTCAACATACCAAACTGTCA 300  
DB 298 TCCAGAAGTCATGGGCGCTACCTCCAAAGTGTCAAAGCATCTCAACATACCAAACTGTCA 357  
QY 301 TGGAAACAGATGGCCACCATCCAGGACTCATATACCAGACGGGAACCTGATAGTCCAA 360  
DB 358 TGGAAACAGATGGCCACCATCCAGGACTCATATACCAGACGGGAACCTGATAGTCCAA 417  
QY 361 TTCCCTGGCTGTGACTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
DB 418 TTCCCTGGCTGTGACTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 477  
QY 421 TCTGTGGACCTGCATTTGACGCTCTCATCAATTTCAAGATCAAAAGACGACGCTTGGA 480  
DB 478 TCTGTGGACCTGCATTTGACGCTCTCATCAATTTCAAGATCAAAAGACGACGCTTGGA 537  
QY 481 ACAGTGTGAGTCTGGAGTTGAGATGAGAACATCTACAGAACTCTCTCTCAGTCTTTTG 540  
DB 538 ACAGTGTGAGTCTGGAGTTGAGATGAGAACATCTACAGAACTCTCTCTCAGTCTTTTG 597  
QY 541 CTGCATTACTACAGTCAACTTACCATCATCATGAGGCTGATATTTCCAGTATGTG 600  
DB 598 CTGCATTACTACAGTCAACTTACCATCATCATGAGGCTGATATTTCCAGTATGTG 657  
QY 601 GATACAAACACTTTCCCTCTTGTATAATGTGCTATCCGCTCTCTTATATAGTACGCTCAGAC 660  
DB 658 GATACAAACACTTTCCCTCTTGTATAATGTGCTATCCGCTCTCTTATATAGTACGCTCAGAC 717  
QY 661 TGA 663

Db 718 TGA 720  
RESULT 8  
US-09-079-785-5  
Sequence 5, Application US/09079785  
Patent No. 6143869  
GENERAL INFORMATION:  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
APPLICANT: Armitage, Richard J.  
APPLICANT: Gruss, Hans-Jurgen  
TITLE OF INVENTION: No. 6143869el Cytokine That Binds CD30  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,785  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,989  
FILING DATE: 12 APRIL 1994  
APPLICATION NUMBER: US 07/966,775  
FILING DATE: 27-OCT-1992  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 720 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: mucD30-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..720  
US-09-079-785-5

Query Match 100.0%; Score 663; DB 3; Length 720;  
Best Local Similarity 100.0%; Pred. No. 2.5e-209;  
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCAGGTGCAGCCCGCTCGGTAGCCAGCCCTGGAGAGACGAGGCGCTCGAGAACG 60  
DB 58 ATGCAGGTGCAGCCCGCTCGGTAGCCAGCCCTGGAGAGACGAGGCGCTCGAGAACG 117  
QY 61 ACAAGTCGCGAGTACTTCTACCTCAGCACCACCGCACTGTGTGCGCTGTGTGGCAGTG 120  
DB 118 ACAAGTCGCGAGTACTTCTACCTCAGCACCACCGCACTGTGTGCGCTGTGTGGCAGTG 177  
QY 121 GCGATCATTCTGGTACTGTAGTCCAGAAAAAGGACTCCCACTCCAATACAACTGAGAAG 180  
DB 178 GCGATCATTCTGGTACTGTAGTCCAGAAAAAGGACTCCCACTCCAATACAACTGAGAAG 237  
QY 181 GCCCCCCCTAAAGGAGGAATGCTCAGAGGATCTCTGTGACCTGAAAGTACTCCA 240  
DB 238 GCCCCCCCTAAAGGAGGAATGCTCAGAGGATCTCTGTGACCTGAAAGTACTCCA 297  
QY 241 TCCAAAGAGTCAATGGCCCTACCTCCAAAGTGTCAAGCATCTCAACAACTGTC 300  
DB 298 TCCAAAGAGTCAATGGCCCTACCTCCAAAGTGTCAAGCATCTCAACAACTGTC 357  
QY 301 TGGAAAGAGTGGCACCACATCCAGGACTCATATACAGGAGGGAACCTGATAGTCCAA 360  
DB 358 TGGAAAGAGTGGCACCACATCCAGGACTCATATACAGGAGGGAACCTGATAGTCCAA 417  
QY 361 TTCCTGGCTTGTACTTCATCGTTTGCCAACTGCAAGTCTCTGTCAGTGCCTCAAAATCAT 420  
DB 418 TTCCTGGCTTGTACTTCATCGTTTGCCAACTGCAAGTCTCTGTCAGTGCCTCAAAATCAT 477  
QY 421 TCTGTGGACCTGACATTCGAGCTCTCATCAATTCAGATCAAAAGCAGAGCTGGTA 480  
DB 478 TCTGTGGACCTGACATTCGAGCTCTCATCAATTCAGATCAAAAGCAGAGCTGGTA 537  
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DB 538 ACAGTGTGTGAGTGTGGAGTTCAGAGTAGAACAATCTACCAAGTCTCTCAGTGTGG 597  
QY 541 CTGCAATTACTTACAGGTCAACTCTACCATATCAGTCAGGCTGGATAATTTCCAGTATGTG 600  
DB 598 CTGCAATTACTTACAGGTCAACTCTACCATATCAGTCAGGCTGGATAATTTCCAGTATGTG 657  
QY 601 GATACAAACACTTTCCCTCTGATATGTCATCGCTTCCTTATATAGTAGCTCAGAC 660  
DB 658 GATACAAACACTTTCCCTCTGATATGTCATCGCTTCCTTATATAGTAGCTCAGAC 717  
QY 661 TGA 663  
DB 718 TGA 720

## RESULT 9

US-08-225-989-22  
Sequence 22, Application US/08225989  
Patent No. 5480981  
GENERAL INFORMATION:  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
APPLICANT: Armitage, Richard J.  
APPLICANT: Gruss, Hans-Jurgen  
TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,989  
FILING DATE: 12 APRIL 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/966,775  
FILING DATE: 27-OCT-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 648 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
IMMEDIATE SOURCE:  
CLONE: huCD30-L  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..648  
US-08-225-989-22

Query Match 60.7%; Score 402.2; DB 1; Length 648;  
Best Local Similarity 79.0%; Pred. No. 3.3e-123;

Matches 492; Conservative 0; Mismatches 128; Indels 3; Gaps 1;

QY 44 CGAGGCCCTGGAGAGCAGACAAAGTCGCGAGCTACTTCTACCTCAGGACCAACCGCACTGG--- 100  
DB 26 CCAGCCACCTGGGGACCAACGAGCGCAGCTATTTCTATTGACCACAGCCACTCTGGCTC 85  
QY 101 TGTGCTCTGTGTGGGAGTGGCGATCATCTGTGCTAGTGTAGTCCAGAAAAAGACTCCA 160  
DB 86 TGTGCTCTGTGTGGGAGTGGCGATCATTTATGTTGTTGGTCTCAGAGGACGACTCCA 145  
QY 161 CTCCAATACAACTGAGAGGCGCCCTTAAAGGAGGAAATTTGCTCAGAGGATCTTTCT 220  
DB 146 TTCCCAACTCACCTGACACAGTCCCTTCAAGGAGGAAATTTGCTCAGAGGACCTTTAT 205  
QY 221 GTACCTGAAAGTACTTCCATCAAGAGTCTACCTGCGGCTTCCCAAGTGTCAAGATC 280  
DB 206 GTATCTGAAAGAGTCTTCAATCAAGAGTCTACCTGCGGCTTCCCAAGTGTCAAGATC 265  
QY 281 TCAACAATACCAACTCTCATGGAACGAGATGCAACCTCAGGACTCATATACAGG 340  
DB 266 TAAACAAACCAAGTGTCTTGTGAACAAAGATGCAATTTCCATGTGAGTGCAGATATCAGG 325  
QY 341 ACGGGAACCTGATAGTCCCAATTCCTGCTGTGACTTTCATCTGTTTGCCTCAACTGCAGTTCC 400

Db 326 ATGGGAATCTGCTGATCCAAATCCCTGGTTTGTACTTCAATTTGCCAACTCAGATTTC 385  
Qy 401 TCGTCAGTGTCAAAATCAATTCCTGGAGCTGACATTTGACGCTCCTCATCAATTTCCAAGA 460  
Db 386 TTGTACAATGCCCAATAAATTTCTGTCGATCTGAAGTTGGAGCTTCTCATCAACAAGCATA 445  
Qy 461 TCAAAAAGCAGAGCTGGTGAACAGTGTGTGAGTCTGAGTCTGAGTTCAGAGTAAAGAACATCTACC 520  
Db 446 TCAAAAAGCAGGCCCTGGTGACAGTGTGTGAGTCTGGAATGCAAAAGCAACAGTATACC 505  
Qy 521 AGAATCTCTCTCAGTTTTTGGCTGCATTACTTACAGTCAACTCTACCATATCAGTCAGG 580  
Db 506 AGAATCTCTCTCAATCTTGGCTGGATTACTTGCAGTCAACACCACTATCAGTCAATG 565  
Qy 581 TGGATAAATTCAGATATGAGTATACAAACACTTTCCCTCTGTGATAATGTCTATCCGTCT 640  
Db 566 TGGATACATTTCCAGTACATAGATACAAAGCACCCTTCTCTTGAGAATGTGTGTCATCT 625  
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Db 626 TCTTATACAGTAATTCAGACTGA 648

## RESULT 10

US-08-570-923-22  
; Sequence 22, Application US/08570923  
; Patent No. 5677430  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armistage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/570,923  
; FILING DATE: 12-DEC-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 648 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; IMMEDIATE SOURCE:  
; CLONE: huCD30-L  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..648  
; US-08-570-923-22

Query Match 60.7%; Score 402.2; DB 1; Length 648;  
Best Local Similarity 79.0%; Pred. No. 3.3e-123;  
Matches 492; Conservative 0; Mismatches 128; Indels 3; Gaps 1;  
Qy 44 CGAGGCCCTGGAGAAGCACAAGTCGCTACTTCTACTCGACACACCGCAGCTGG--- 100  
Db 26 CCAGCCACTGGGACCCAGAGCCGACGCTATTCTATTGACCACGCCACTCTGGGTC 85  
Qy 101 TGTGCTTGTGTTGGCAGTGGCGATCATTTCTGGTACTGTGTATGTCAGAAAAAGGACTCCA 160  
Db 86 TGTGCTTGTCTTCAGGGTGGCCACTATTATGTTGTTGTTGTTTCAGAGGAGGACTCCA 145  
Qy 161 CTCGAATACAACTGAGAAGGCCCCCTTTAAAGAGGAAATTTGTCAGAGGATCTCTTCT 220  
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Qy 221 GTACCTCAAAAGTACTCCATCCAAAGAGTCATGGCCCTACTCCCAAGTGTCAAGATC 280  
Db 206 GTATCTGAAAAGAGCTCCATTCAAGAAAGTCATGGGCCCTACTCTCAAGTGGCAAGCATC 265  
Qy 281 TCAACAATACCAAACTGTCTATGGAAAGAGATGGCACCATCCAGGACTCATATACCAAG 340  
Db 266 TAACAAAACCAAGTTGCTTTGGAACAAGATGGCATTTCTCCATGGAGTCAGATATCAGG 325  
Qy 341 ACGGAACCTGATAGTCCAAATTCCTGGCTGTGTTACTTTCATCGTTGGCCAACTGCAAGTCC 400  
Db 326 ATGGGAATCTGCTGATCCAAATTCCTGGTGTGTTACTTTCATCATATTGGCCAACTGCAAGTTC 385  
Qy 401 TCGTGCAGTGTCTCAAAATCATTTCTGTGGACCTGACATTTGCAGCTCCTCATCAATTC 460  
Db 386 TTGTACAATGCCCAAAATAATTTCTGCGATCTGAAGTTGGAGCTTCTCATCAACAAGCATA 445  
Qy 461 TCAAAAAGCAGACGTTGGTAAACAGTGTGTGAGTCTGGAGTTTCAGAGTAAAGAACATCTACC 520  
Db 446 TCAAAAACAGGCCCTGGTGACAGTGTGTGAGTCTGGAAATGCAAAACGAAACACGTAATACC 505  
Qy 521 AGAATCTCTCAGTTTTTGTGCTGCAATTTACAGGTCAACTCTACCATATCAGTCAGG 580  
Db 506 AGAATCTCTCAATTTCTGCTGGATTACCTGCAGTCAACACCACTATCAGTCAATG 565  
Qy 581 TGGATAATTTCCAGTATGTTGATACAAACACTTTCCCTCTTGTGATAATGTCTATCCGTCT 640  
Db 566 TGGATACATTTCCAGTACATAGATACAAAGCACCCTTCTCTTGTGAGAATGTGTGTCATCT 625  
Qy 641 TCTTATATAGTACCTCAGACTGA 663  
Db 626 TCTTATACAGTAATTCAGACTGA 648

## RESULT 11

US-08-580-014-22  
; Sequence 22, Application US/08580014  
; Patent No. 5753203  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.



Qy	161	CTCAAATACAATGAGAGGCCCCCTTAAAGAGGAGAAATTGCTCAGAGGATCTCTTCT	220
Db	146	TTCCCAACTCACCTGACAAAGTCCCCCTCAAAGGAGGAAATTGCTCAGAAGACCTTTAT	205
Qy	221	GTACCCTGAAAGTACTCCATCCAAGAGTCATGGCCCTACCTCCAAGTGTCAAAGCATC	280
Db	206	GTATCTTGAAGAGCTCCATTCAGAAGTTCATGGGCCCTACCTCCAAGTGGCAAGCATC	265
Qy	281	TCAACAAATACCAAACTGTCTATGGAAGGAAGATGGCAACCATCCACGGACTCATATACGAG	340
Db	266	TAAACAAACCAAGTTGCTTTGGAACAAAGATGGCATTTCCATGGAGTCAGATATCAGG	325
Qy	341	ACGGGAACCTGATAGTCCAAATCCCTGGCCTTGTTACTTCATCGTTTGCCAACTGCAGTTCC	400
Db	326	ATGGGAATCTGGTGATCCAAATCCCTGGTTGTGTACTTCATCATTTTGCCAACTGCAGTTTC	385
Qy	401	TCGTGCAGTGCCTCAAAATCAATCTGTGGACCTGCACATTCGAGCTCCCTCATCAATCCCAAGA	460
Db	386	TTGTACAAATGCCCAATAATCTGTGCATGGAAGTTGGAGCTTCATCAACAAAGCATAT	445
Qy	461	TCAAAAAGCAGAGCGTTGGTAACAGTGTGTGAGTCTGGAGTTCAGAGTAAGAACATCTACC	520
Db	446	TCAAAAACAGGCCCTGGTGACAGTGTGTGAGTCTGGAATGCAAAAGCAACACGATATACC	505
Qy	521	AGAACTCTCTCAGTTTTTCTGCTGCATTTACTTACAGTGTCAACTCTACCATATCAGTCAGGG	580
Db	506	AGAACTCTCTCAATTTCTGCTGGATTAACCTGCAGGTCAACACCACTATCAGTCAATG	565
Qy	581	TGGATAATTTTCCAGTATGTGGATCAAAACACTTTCCCTCTTGATAATTTGCTATCCGTCT	640
Db	566	TGATACATTTCCAGTACATAGATACAAGACCTTTCTCTTGAAATGTGTCTCCATCT	625
Qy	641	TCTATATATAGTACTCAGACTGA	663
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		Query Match	60.7%;	Score 402.2;	DB 1;	Length 648;	
		Best Local Similarity	79.0%;	Pred. No. 3.3e+123;			
		Matches 492;	Conservative 0;	Mismatches 128;	Indels 3;	Gaps 1;	
QY	44	CGAGGCCCTGGAGAACACAAAGTCGACGTACTTCTTACTCAGCACACCACGCACATGG---	100				
Dd	26	CCAGCCACCTGGGACCACGAGCGCAGCTATTCTTATTTGACCACACGCCACTCTGGCTC	85				
QY	101	TGTGCCCTGTTGTGGCAGTGCGCATATCTTCGGTACTGGGTAGTCAGAAAAAGGACTCCA	160				
Dd	86	TGTGCCCTTGTCTTCACGGTGCCCACTATTATNGTGTGGTCTGTCAGAGGACGGACTCCA	145				

;; FILING DATE: 01-JUL-1992  
;; PRIOR APPLICATION DATA: US 899,660  
;; FILING DATE: 15-JUN-1992  
;; PRIOR APPLICATION DATA: US 892,459  
;; FILING DATE: 02-JUN-1992  
;; PRIOR APPLICATION DATA: US 889,717  
;; FILING DATE: 26-MAY-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Seese, Kathryn A.  
;; REGISTRATION NUMBER: 32,172  
;; REFERENCE/DOCKET NUMBER: 2804-E  
;; TELEPHONE: (206)587-0430  
;; TELEFAX: (206)233-0644  
;; TELEX: 756822  
;; INFORMATION FOR SEQ ID NO: 22:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 648 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: cDNA to mRNA  
;; IMMEDIATE SOURCE:  
;; CLONE: huCD30-L  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 1..648  
US-09-079-785-22

Query Match 60.7%; Score 402.2; DB 3; Length 648;  
Best Local Similarity 79.0%; Pred. No. 3.3e-123;  
Matches 492; Conservative 0; Mismatches 128; Indels 3; Gaps 1;  
QY 44 CGAGCCCTGGAGACGACAGTCGAGCTACTTCTACCTCAGCAGCCGCGACTGG--- 100  
DB 26 CGAGCCACTGGGGACCGAGCGCGAGCTATTCTTATTTGACACGAGCCACTCTGGCTC 85  
QY 101 TGTGCTTTGTTGGCAGTGGGGATCTTCTGGTACTGGTAGTCCAGAAAAAGACTCCA 160  
DB 86 TGTGCTTTGTTCTGCTGAGTGGGCACTATTATGTTGTTGCTGTCAGAGCGAGCTCCA 145  
QY 161 CTCGAAATACAACTGAGAGGCGCCCTTAAAGGAGGAAATTCCTCAGAGGATCTCTCT 220  
DB 146 TCCCAACTCCTGACAAACGTCCTCCCTCAAGGAGGAAATTCCTCAGAGGACTCTTAT 205  
QY 221 GTACCTGAAAGTACTCCATCCAGAGTCTGATGGGCTTACCTCCAAAGTGTCAAAGCATC 280  
DB 206 GTATCCTGAAAGAGCTCCATTCAAGAGTCTGATGGGCTTACCTCCAAAGTGGCAAGCATC 265  
QY 281 TCAACAATACCAAGTGTGATGGAAGAGATGGGACCATCCACGACATCATATACAGG 340  
DB 266 TAAACAAAACCAAGTGTCTTGAACAAAGATGGCATTCCTCATGAGTACAGATATCAGG 325  
QY 341 ACGGAACTGATAGTCCAAATTCCTGGCTTGTACTTCATCTGTTTCCCACTCAGTTCC 400  
DB 326 ATGGGAATCTGTTGATCCAAATTCCTGGTGTGTACTTCATCTATTTGCCAACTCAGTTTC 385  
QY 401 TCGTCAGTGTCTCAATCTTCTGTGGACTGACATTCGAGTCCCTCATCAATTTCCAAGA 460  
DB 386 TTGTACATGCCCAATAATATCTGTGCATCTGAGTTGGAGCTTCATCAACAAGCAT 445  
QY 461 TCAAAAGCAGACGTTGGTAAAGTGTGTGAGTCTGAGTTTCAAGTTCAGAGTAAAGACATACC 520  
DB 446 TCAAAAGCAGACGCTGGTGGACAGTGTGTGAGTCTGGAATGCAACGAAACAGATATACC 505  
QY 521 AGAATCTCTCAGTTTGTGTCATTTACTTACAGTGTCAACTTACCATATCAGTCAGG 580  
DB 506 AGAATCTCTCAATTTCTGCTGGATTACCTGCGAGTCAACACCACTATCATGCAATG 565

QY 581 TGGATAATTTCCAGTATGTGGATACAAACACTTTCCCTCTTTGATAAATGTGCTATCCGCT 640  
DB 566 TGGATACATTTCCAGTATGATAGATACAGCACTTTCTCTTTGAGAAATGTGTTGCTCATCT 625  
QY 641 TCTTATAGTAGTCTCAGACTGA 663  
DB 626 TCTTATACAGTAATTCAGACTGA 648  
RESULT 13  
US-08-225-989-7  
; Sequence 7, Application US/08225989  
; Patent No. 5480981  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 705 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA to mRNA  
; IMMEDIATE SOURCE:  
; CLONE: huCD30-L  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..705  
US-08-225-989-7

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Query Match      60.7%; Score 402.2; DB 1; Length 705;
Best Local Similarity 79.0%; Pred. No. 3.5e-123;
Matches 492; Conservative 0; Mismatches 128; Indels 3; Gaps 1;

Qy 44 CGAGCCCTGGAGAGCACAAGTCGAGCTACTTCTTACCTCAGCACCACCGCACTGG--- 100
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Qy 101 TGTGCTTGTGTCGAGTGGGATCATCTCTGCTAGTCTCAGAGAAAGGACTCCA 160
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Db 143 TGTGCTTGTGTCGAGTGGGATCATCTCTGCTAGTCTCAGAGAAAGGACTCCA 202
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Qy 161 CTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 220
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Db 203 TTCCCACTACCTGACACGCTCCCTCCAAAGGAGAAATGCTCAGAGACCTCTTAT 262
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Qy 221 GTACCTGAAAGTACTCCATCAAGAGAGTATGAGGCTTACCTCCAAAGTGTCAAAGCATC 280
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Qy 281 TCAACAATACCAAGTGTGCTGAGAGAGTGTGAGGCTTACCTCCAAAGTGTCAAAGCATC 340
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Db 323 TAAACAATACCAAGTGTGCTGAGAGAGTGTGAGGCTTACCTCCAAAGTGTCAAAGCATC 382
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Qy 341 ACGGAACTGATAGTCCAAATCCCTGGCTTGTACTTCTGCTGCTGCTGCTGCTGCTGCT 400
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Db 383 ATGGAACTGATAGTCCAAATCCCTGGCTTGTACTTCTGCTGCTGCTGCTGCTGCTGCT 442
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Qy 401 TCGTGCAGTGTCAATCATCTGTGAGAGTGTGAGGCTTACCTCCAAAGTGTCAAAGCATC 460
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Qy 461 TCAAAAAGCAGCTGTGTAACAGTGTGAGTGTGAGGCTTACCTCCAAAGTGTCAAAGCATC 520
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Db 503 TCAAAAAGCAGCTGTGTAACAGTGTGAGTGTGAGGCTTACCTCCAAAGTGTCAAAGCATC 562
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Qy 641 TCTTATATAGTACGACTGA 663
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RESULT 14
US-08-570-923-7
; Sequence 7, Application US/08570923
; Patent No. 5677430
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jürgen
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1

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; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,923
; FILING DATE: 12-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 705 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; IMMEDIATE SOURCE:
; CLONE: huCD30-L
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..705
; US-08-570-923-7

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Query Match      60.7%; Score 402.2; DB 1; Length 705;
Best Local Similarity 79.0%; Pred. No. 3.5e-123;
Matches 492; Conservative 0; Mismatches 128; Indels 3; Gaps 1;

Qy 44 CGAGCCCTGGAGAGCACAAGTCGAGCTACTTCTACCTCAGCACCACCGCACTGG--- 100
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 83 CGAGCCACCTGGGACGACGAGCCGAGCTATTCTATTGACGACGCACTCTGGCTC 142
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 101 TGTGCTTGTGTCGAGTGGGATCATCTCTGCTAGTCTCAGAGAAAGGACTCCA 160
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Db 143 TGTGCTTGTGTCGAGTGGGATCATCTCTGCTAGTCTCAGAGAAAGGACTCCA 202
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Qy 161 CTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 220
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Db 203 TTCCCACTACCTGACACGCTCCCTCCAAAGGAGAAATGCTCAGAGACCTCTTAT 262
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy 221 GTACCTGAAAGTACTCCATCAAGAGAGTGTGAGGCTTACCTCCAAAGTGTCAAAGCATC 280
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[illegible]

RESULT 15  
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; Sequence 7, Application US/08580014  
; Patent No. 5753203  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Immiteage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/580,014  
; FILING DATE: 20-DEC-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430

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; TELEFAX: (206)233-0644
;
; TELEX: 756822
;
; INFORMATION FOR SEQ ID NO: 7:
;
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 705 base pairs
;     TYPE: nucleic acid
;     STRANDEDNESS: single
;     TOPOLOGY: linear
;     MOLECULE TYPE: cDNA to mRNA
;     IMMEDIATE SOURCE:
;     CLONE: hucD30-L
;     FEATURE:
;         NAME/KEY: CDS
;         LOCATION: 1..705
;
; US-08-580-014-7

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Query Match	50.7%	Score 402.2	DB 1	Length 705
Best Local Similarity	79.0%	Pred. No. 3.5e-123		
Matches 492	Conservative 0	Mismatches 128	Indels 3	Gaps 1
QY 44	CGAGGCCCTGGAGAAGCACAAAGTCGACGCTACTTCTACCTCAGCACACCACGCACTGG---100			
Db 83	CCAGCCACCTGGGACCACAGCGCGACGCTAATTTCTATTGACCACACGCCACTCTGGCTC 142			
QY 101	TGTGCCCTTGTTGGCAGTGGCGATCATCTTCGTGCTACTGGTAGTCGAGAAAAGGAACTCCA 160			
Db 143	TGTGCCCTTGCTTCACGGTGGCCACTATTATGGTGTGGTCTGTCAGAGGACGAACTCCA 202			
QY 161	CTCCAAATACAACCTGAGAAGGCCCCCTTAAAGAGGAAATTTGCTCAGAGGACTCTTTCT 220			
Db 203	TTCCCAACTCACCTGCAACACGCTCCCTTCAAAGGAGGAAATTTGCTCAGAGACCTCTTAT 262			
QY 221	GTACCCGTAAAGTACTCCATCCAAGAAGTCATGGGCCCTACTCTCAAAGTGTCAAAAGCATC 280			
Db 263	GTATCCTGAAAGAGCTCCATTTCAGGAAGTCATGGGCCCTACTCTCCAAGTGGCAAGCATC 322			
QY 281	TCACAATATCCAAACTGTCATGGAAAGGAAGATGCACCATCCAGCGACTCATATACCAAGG 340			
Db 323	TAAACAACCAAGTTGTCTTGGACAAAGATGGCATCTCCNTGGAGTCAGATATACAGG 382			
QY 341	ACGGGAACCTGATAGTCCAAATTCCTGGCTGTGTACTTCACTGTTTGGCAACTCGAGTTCC 400			
Db 383	ATGGGAATCTGGTGATCCAAATTCCTGGTTGTACTTTCATCATCTTGGCAACTCGAGTTTC 442			
QY 401	TCGTGCGAGTGTCAAAATCATTTCTGTGGACCGACATGTCAGCTCCTCATCAATTCACAAG 460			
Db 443	TTGTACAATGCCCAATAAATCTCTCGATCTGGAATCTGGAGCTTCTCATCAACAAGCATATA 502			
QY 461	TCAAAAGACGACGTTGGTACAGTGTCTGAGTCTGGAGTTTCAGAGTAAAGAACATCTACC 520			
Db 503	TCAAAAGACGCGCCTGGTGACAGTGTGTGAGTCTGGAAATCAACACGAAACACGATATACC 562			
QY 521	AGAATCTCTCTCAGTTTTTGGCTGCATTACTTACAGGTTCAACTCTACCATATCAGTCAGGG 580			
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Db 623	TGGATACATTTCCAGTACATAGATCAAGCACCTTTTCCTCTTGTGAGAAATGTGTTGCCACTCT 682			
QY 641	TCATTATATAGTAGCTACAGTGA 663			
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Job time: 9904 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 5, 2001, 23:43:12 ; Search time 111.92 Seconds  
(without alignments)  
3719.610 Million cell updates/sec

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Perfect score: 663

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Gapop 10.0 , Gapext 1.0

Searched: 730101 seqs, 313950809 residues

Total number of hits satisfying chosen parameters: 1460202

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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#### SUMMARIES

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7	402.2	60.7	1906	19	AAV39012
8	42.6	6.4	936	22	AAF58252
c 9	42.6	6.4	936	22	AAF58252
10	42.6	6.4	936	22	AAF58254
c 11	42.6	6.4	936	22	AAF58254

c 12	42.6	6.4	936	22	AAF58257	Oligonucleotide D1
c 13	42.6	6.4	936	22	AAF58257	Oligonucleotide D1
c 14	42.6	6.4	936	22	AAF58259	Oligonucleotide D2
c 15	42.6	6.4	936	22	AAF58259	Oligonucleotide D2
c 16	42.6	6.4	936	22	AAF58262	Oligonucleotide D2
c 17	42.6	6.4	936	22	AAF58262	Oligonucleotide D2
c 18	42.6	6.4	938	22	AAF58255	Oligonucleotide D1
c 19	42.6	6.4	938	22	AAF58255	Oligonucleotide D1
c 20	40.4	6.1	1031	21	AAC47628	Arabidopsis thalia
c 21	40.4	6.1	1100	21	AAC49976	Arabidopsis thalia
c 22	38.8	5.9	1036	21	AAC36192	Arabidopsis thalia
c 23	38.8	5.9	1105	21	AAC37173	Arabidopsis thalia
c 24	38.8	5.9	1342	21	AAC52167	Arabidopsis thalia
c 25	34.4	5.2	4356	16	AAQ95540	Cardiac adenyl c
c 26	34.2	5.2	379	21	AAC00135	Human secreted pro
c 27	34.2	5.2	1432	19	AAV21689	DNA encoding a hum
c 28	34.2	5.2	1433	19	AAV13925	Human cartilage gp
c 29	34.2	5.2	1496	18	AAV97127	Human cartilage gl
c 30	33.6	5.1	509	21	AAC08862	Human secreted pro
c 31	33.4	5.0	1886	22	AAF92535	Rat T2R08 nucleoti
c 32	33.2	5.0	3768	21	AAC81955	Human Meg-3 cDNA.
c 33	32.8	4.9	1403	21	AAC36591	Arabidopsis thalia
c 34	32.8	4.9	4356	14	AAQ37543	Cardiac adenyl c
c 35	32.4	4.9	1038602	20	AAZ01425	Complete genome se
c 36	32.2	4.9	1467	21	AAC78872	Human ORF2427
c 37	32	4.8	1526	19	AAV13926	Human cartilage gp
c 38	32	4.8	1594	19	AAV21687	DNA encoding a hum
c 39	32	4.8	1594	19	AAV21688	DNA encoding a hum
c 40	32	4.8	26016	19	AAV52722	Human flavin-conta
c 41	31.4	4.7	1205	22	AAC85551	cDNA encoding CDIF
c 42	31.4	4.7	1314	21	AAC44675	zea mays DNA fragm
c 43	31.2	4.7	374	21	AAA51168	Hybrid 7 transmemb
c 44	31.2	4.7	3428	19	AAV24138	Homo sapiens BAP15
c 45	31.2	4.7	3517	19	AAV18626	Homo sapiens BRCA1

#### ALIGNMENTS

RESULT 1	
AAQ53535	
ID	AAQ53535 standard; cDNA; 663 BP.
XX	
AC	AAQ53535;
XX	
DT	19-JUN-1994 (first entry)
XX	
DE	Sequence of the coding region of a murine CD30-L cDNA clone.
XX	
KW	Hodgkin's disease; lymphoma; surface antigen; cytokine;
KW	CD30 ligand; CD30-L; TNF; NGF; ss.
XX	
OS	Acomys cahirinus.
XX	
FH	Key
FT	CDS
FT	Location/Qualifiers
FT	1..663
XX	/*tag= a
XX	
PN	WO9324135-A.
XX	
PD	09-DEC-1993.
XX	
PF	25-MAY-1993; 93WO-US04926.
XX	
PR	26-MAY-1992; 92US-0889717.
PR	02-JUN-1992; 92US-0892459.
PR	15-JUN-1992; 92US-0899660.
PR	01-JUL-1992; 92US-0907224.
PR	27-OCT-1992; 92US-0966775.
XX	(IMV ) IMMUNEX CORP.
PA	
XX	Armitage RJ, Goodwin RG, Smith CA;
PI	

XX WPI; 1993-405417/50.  
 DR P-PSDB; AAR45006.  
 XX  
 PT New cytokine, CD30-L, which binds CD30 - used for developing  
 PT prods. for diagnosis, detection, purifications, research and  
 XX therapy  
 XX  
 PS Claim 1; Figure 3a; 59pp; English.  
 XX  
 CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used  
 CC as a clinical marker for Hodgkin's lymphoma and related haematologic  
 CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-  
 CC L and other derived prods. can be used for elucidating the roles  
 CC that CD30 and CD30-L may play in the immune system and for diagnosis  
 CC and therapy. It can be isolated as follows. A cDNA library prep'd from  
 CC the murine helper T-cell line 7B9 is screened with a CD30/FC fusion  
 CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L.  
 CC This cDNA can then be used as a probe to screen a human PBL cDNA  
 CC library to obtain cDNA encoding human CD30-L.  
 XX  
 SQ Sequence 663 BP; 180 A; 175 C; 144 G; 164 T; 0 other;

Query Match 100.0%; Score 663; DB 14; Length 663;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-200;  
 Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCAGGTGCAGCCGGCTCGGTAGCCGCCCTTGAGAGCAGAGGCCCTGGAGAGC 60  
 DB 1 atgcagggtgcagccggctcggttagccgcccttgagagcagagggccctggagaagc 60  
 QY 61 ACAAGTCCAGCTACTTCTACCTCAGCACCACCGCACTGGTGTGCTTGTGGCAGTG 120  
 DB 61 acaagtccagctacttctacctcagcaccacgcagcactgggtgtgcttgtggcagtg 120  
 QY 121 GCGATCATCTGGTACTGGTAGTCCAGAAAAAGGACTCCCACTCAATAACAAGTGAAG 180  
 DB 121 gcgatcattctggtactggttagtccagaaaaaggactccctcccaataacaagtgaag 180  
 QY 181 GCCCCCTTAAGGAGGAAATGCTCAGAGGATCTTCTGTACCTGAAAAGTACTCCA 240  
 DB 181 gccccccttaaggaggaaatgctcagaggatcttctgtaccctgaaaagtactcca 240  
 QY 241 TCCAGAAAGTCAATGGCTTACCTCCAAAGTGTCAAAGCATCTCAACAATACCAACTGTCA 300  
 DB 241 tccagaaagtcaatggcttacctccaaagtgtcaaagcatctcaacaataccaactgtca 300  
 QY 301 TGGACGAGATGGCACCATCCACGACTCATATACAGGAGGGAACTGATAGTCCAA 360  
 DB 301 tggacgagatggcaccatccacgactcatatacaggagggaaactgatatagtccea 360  
 QY 361 TTCCTGGCTGTACTTCAATCGTTTGGCACTGCAAGTCCAGTTCCTGTGAGTGCCTCAATCAT 420  
 DB 361 ttcctggctgtacttcaatcgtttggcactgcaagtccagttcctgtgagtgctcaatcat 420  
 QY 421 TCTGTGACCTGACATTCAGCTCCTCATCAATTCAGATCCAAAGCAGAGCTTGGTA 480  
 DB 421 tctgtgacctgacattcagctcctcatcaattcagatccaaagcagagcttggta 480  
 QY 481 ACAGTGTGTAGTCTGGAGTTTCAGAGTAAGAACATCTACAGAAATCTCTCTCAGTFTTTG 540  
 DB 481 acagtgtgtagtctggagtttccagagtaagaaacatctacagaaatctctcagfttttg 540  
 QY 541 CTGATTTACTTTACAGGTCAACTCTACCATATACAGTCAGGGTGGATAAATTTCCAGTATGTG 600  
 DB 541 ctgatTTACTTTACAGGTCAACTCTACCATATACAGTCAGGGTGGATAAATTTCCAGTATGTG 600  
 QY 601 GATACAAACACTTTCCCTTTGATATGCTATCCGCTTCTTATATAGTACTCAGAC 660  
 DB 601 gatacaacactttccctttgatatgctatccgcttcttataatagtagtactcagac 660  
 QY 661 TGA 663

Db 661 tga 663

# RESULT 2

AAV42207  
 ID AAV42207 standard; DNA; 720 BP.

XX  
 AC AAV42207;

XX  
 DT 23-SEP-1998 (first entry)

XX  
 DE CD30 ligand gene used in the course of the invention.

XX  
 KW CD30 ligand; alteration; immunoreactivity; human cell;  
 KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;  
 KW autoimmune disorder; rheumatoid arthritis; vaccine; ss.

XX  
 OS Mus sp.

XX  
 PN WO9826061-A2.

XX  
 PD 18-JUN-1998.

XX  
 PF 08-DEC-1997; 97WO-US22740.

XX  
 PR 01-DEC-1997; 97US-0982272.

XX  
 PR 09-DEC-1996; 96US-0032145.

XX  
 PA (REGC ) UNIV CALIFORNIA.

XX  
 PI Cantwell M, Kipps TJ, Sharma S;

XX  
 DR WPI; 1998-348521/30.

XX  
 PT Vectors containing accessory molecule ligand genes - used for  
 PT altering immunoreactivity of cells, particularly for treatment of  
 PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis  
 XX  
 PS Disclosure; Page 125; 167pp; English.

CC The present sequence represents a CD30 ligand gene. The sequence is  
 CC used to exemplify the method of the invention. The specification  
 CC describes a method for altering the immunoreactivity of human cells  
 CC which comprises introducing a gene encoding an accessory molecule  
 CC ligand (AML) into the cells so that the AML is expressed on the surface  
 CC of the cells. Vectors containing the AML genes can be used in gene  
 CC therapy for treating neoplasia or autoimmune disorders such as rheumatoid  
 CC arthritis. They can also be used for vaccination to produce immunity  
 CC against a virus cell, bacteria, protein, fungus or neoplasia.

XX  
 SQ Sequence 720 BP; 191 A; 195 C; 162 G; 172 T; 0 other;

Query Match 100.0%; Score 663; DB 19; Length 720;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-200;  
 Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCAGTGCAGCCGGCTCGGTAGCCAGCCCTGGAGAGCAGAGGCCCTGGAGAGC 60  
 DB 58 atgcagggtgcagccggctcggttagccagccctggagaagcagagccctggagaagc 117

QY 61 ACAAGTGCAGCTACTTCTACCTCAGCACCACCGCACTGGTGTGCTTGTGGCAGTG 120  
 DB 118 acaagtgcagctacttctacctcagcaccacccagcactgggtgcttgtgtgagcagt 177

QY 121 GCGATCATCTGGTACTGGTAGTCCAGAAAAGGACTCCACTCCAAAATACAACTGAGAAG 180  
 DB 178 gcgatcattctggtactggttagtccagaaaaagagactccactccaaatacaactgagaag 237

QY 181 GCCCCCCCTTAAGGAGGAAATTTGCTCAGAGGATCTTCTTACCCCTGAAAGTACTCCA 240  
 DB 238 gccccccttaaggaggaaattgtctcagaggtctcttctgtacccctgaaaagtactcca 297

QY 241 TCCAAAGATCATGGCGCTACCTCCCAAGTGTCAAGCATCTCAACATACCAAACTGTCA 300  
|||||  
Db 298 tccaagaagtcattggcgctacctccaagtgtcaaaagcatctcaacaataccaaactgtca 357  
QY 301 TGGACGAAGATGSCACCATCCAGGACTCATATACCAGACGGGAACCTCATAGTCCAA 360  
|||||  
Db 358 tggaaagaagatggcaccatccacggactcatataccagagacgggaacctgatagtcocaa 417  
QY 361 TTCCCTGGCTGTGACTTCATCGCTTTGCAACTGTCAGTTCCTGTCGAGTGTCAAAATCAT 420  
|||||  
Db 418 ttccctggctgtacttcacgtttgccaactgcagttcctcgtgcagtgctcaaatcat 477  
QY 421 TCCTGTGACCTGACATTCGAGTCTCCTCATCAATTCGAAGATCAAAAAGCAGACGTTGGTA 480  
|||||  
Db 478 tctgtggacctgacattgcagctcctcatcaattccaagatccaaagacagacgttggtta 537  
QY 481 ACAGTGTGAGTCTGAGTCTGAGTCAAGTAAGAACATCTACCAAGATCTCTCAGTTTGTG 540  
|||||  
Db 538 acagtggtgagctggagttcagagtaagaacatctaccagaaatctctcagtttttg 597  
QY 541 CTGCATTACTTACAGTTCAACTCTACCATATCAGTCAAGGTTGGATAATTTCCAGTATGTG 600  
|||||  
Db 598 ctgcattactacagtgcaactctacatcatcagtcagtggaataattccagtatgtg 657  
QY 601 GATACAAACACTTTCCCTCTTTGATAATGTGCTATPCCTCTCTTTATATAGTAGTCCAGAC 660  
|||||  
Db 658 gatataaacactttccctcttgataatgtgctatccgtctcttctatatagtagtccagac 717  
QY 661 TGA 663  
|||  
Db 718 tga 720

## RESULT 3

AAV42186  
ID AAV42186 standard; DNA; 1783 BP.

XX AC

XX AC AAV42186;

XX DT 23-SEP-1998 (first entry)

XX DE CD40 ligand gene used in the course of the invention.

XX KW CD40 ligand; alteration; immunoreactivity; human cell;

XX KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;

XX KW autoimmune disorder; rheumatoid arthritis; vaccine; ss.

XX OS Mus sp.

XX PN W09826061-A2.

XX PD 18-JUN-1998.

XX PF 08-DEC-1997; 97WO-0522740.

XX PR 01-DEC-1997; 97US-0982272.

XX PR 09-DEC-1996; 96US-0032145.

XX PA (REGC ) UNIV CALIFORNIA.

XX PI Cantwell M, Kipps TJ, Sharma S;

XX DR WPI; 1998-348521/30.

XX PS Vectors containing accessory molecule ligand genes - used for

XX PT altering immunoreactivity of cells, particularly for treatment of

XX PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis

XX PS Disclosure; Page 117; 167pp; English.

XX CC The present sequence represents a CD40 ligand gene. The sequence is

XX CC used to exemplify the method of the invention. The specification

CC describes a method for altering the immunoreactivity of human cells  
CC which comprises introducing a gene encoding an accessory molecule  
CC ligand (AML) into the cells so that the AML is expressed on the surface  
CC of the cells. Vectors containing the AML genes can be used in gene  
CC therapy for treating neoplasia or autoimmune disorders such as rheumatoid  
CC arthritis. They can also be used for vaccination to produce immunity  
CC against a virus cell, bacteria, protein, fungus or neoplasia.

XX SQ Sequence 1783 BP; 515 A; 411 C; 407 G; 450 T; 0 other;

Query Match 100.0%; Score 663; DB 19; Length 1783;  
Best Local Similarity 100.0%; Pred. No. 5.7e-200;  
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATCAGGTGTCAGCCCGCTCGGTAGCCAGCCCTCGAGAACGACGAGGCCCTGGAGAAGC 60  
|||||  
Db 170 atgcaggtgcagcccgctcggttagccagccctgagagaagcagccctggagaagc 229  
QY 61 ACAAGTCGAGCTACTTCTACCTCAGCACACCGACCTGGTGTGCTTGTGTGGCAGTG 120  
|||||  
Db 230 acaagtcgagctacttctacctcagcaccacgcactggtgctgtgtgtgagcagtg 289  
QY 121 GCGATCACTTCTGGTACTGCTAGTCCAGAAAAGGACTCCACTCCAAATACAACTGAGAAG 180  
|||||  
Db 290 gcgatcatctcgtgtactggttagtcagaaaaagagactccactcccaatacacaactgagaag 349  
QY 181 GCCCCCTTAAAGAGGAGAAATTCCTCAGAGGATCTCTCTGTACCTGAAAAAGTACTCCA 240  
|||||  
Db 350 gccccccttaagaggagaaattgctcagaggatctctctgtaccttgaaagactacca 409  
QY 241 TCCAAAGAGTCAATGGGCTTACCTCCAAAGTGTCAAAAGCATCTCAACAATACCAAACTGTCA 300  
|||||  
Db 410 tccaagaagtcattggcgctacctccaagtgcaaaagcatctcaacaataccaaactgtca 469  
QY 301 TGGACGAAGATGSCACCATCCAGGACTCATATACCAGACGGGAACCTCATAGTCCAA 360  
|||||  
Db 470 tggaaagaagatggcaccatccacggactcatataccagagacgggaacctgatagtcocaa 529  
QY 361 TTCCCTGGCTGTGACTTCATCGCTTTGCCAACTGTCAGTTCCTGTCAGTGTCTCAATCAT 420  
|||||  
Db 530 ttccctggctgtgacttcacgtttgccaactgcagttcctcgtgcagtgctcaaatcat 589  
QY 421 TCTGTGGACCTGACATTCAGCTCCTCATCAATTCCAAGATCAAAAAGCAGACGTTGGTA 480  
|||||  
Db 590 tctgtggacctgacattgcagctcctcatcaattccaagatcaaaagacagactgtgta 649  
QY 481 ACAGTGTGAGTCTGAGTTCGAGTTCAGAGTAAAGACATCTACCAGAAATCTCTCAGTTTGTG 540  
|||||  
Db 650 acagtggtgagctggagttcagagtaagaacatctaccagaaatctctcagtttttg 709  
QY 541 CTGCATTACTTACAGTTCAACTCTACCATATCAGTTCAGGTTGGATAATTTCCAGTATGTG 600  
|||||  
Db 710 ctgcattacttacaggttcaactctaccatacagtcaggggagcaattccagtatgtg 769  
QY 601 GATACAAACACTTTCCCTCTTGTATATGTGCTATCCGCTCTTCTTATATAGTAGTCCAGAC 660  
|||||  
Db 770 gatataaacactttccctcttgataatgtgctatccgtctcttctatatagtagtccagac 829  
QY 661 TGA 663  
|||  
Db 830 tga 832

## RESULT 4

AAQ53537  
ID AAQ53537 standard; cDNA; 720 BP.

XX AC

XX AC AAQ53537;

XX DT 19-JUN-1994 (first entry)

XX DE Sequence of the coding region of a murine CD30-L cDNA clone

DE encoding additional N-terminal amino acids.

KW Hodgkin's disease; lymphoma; surface antigen; cytokine;  
KW CD30 ligand; CD30-L; TNF; NGF; ss.

XX Acromys cahirinus.

XX Key Location/Qualifiers  
FH CDS 1..720  
FT /\*tag= a

XX WO9324135-A.

XX 09-DEC-1993.

XX 25-MAY-1993; 93WO-US04926.

XX 26-MAY-1992; 92US-0889717.

XX 02-JUN-1992; 92US-0892459.

XX 15-JUN-1992; 92US-0899660.

XX 01-JUL-1992; 92US-0907224.

XX 27-OCT-1992; 92US-0966775.

XX (IMMV ) IMMUNEX CORP.

XX Armitage RJ, Goodwin RG, Smith CA;

XX WPI; 1993-405417/50.

XX P-PSDB; AAR45008.

XX New cytokine, CD30-L, which binds CD30 - used for developing  
PT prods. for diagnosis, detection, purifications, research and  
PT therapy

XX Claim 1; Figure 6a; 59pp; English.

XX CD30-L is a ligand for CD30, the 120kd surface antigen widely used  
CC as a clinical marker for Hodgkin's lymphoma and related haematologic  
CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-  
CC L and other derived prods. can be used for elucidating the roles  
CC that CD30 and CD30-L may play in the immune system and for diagnosis  
CC and therapy. It can be isolated as follows. A cDNA library prep. from  
CC the murine helper T-cell line 7B9 is screened with a CD30/FC fusion  
CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L  
CC (AAQ53535). This cDNA can then be used as a probe to screen a human PBL  
CC cDNA library to obtain cDNA encoding human CD30-L (AAQ53536). An  
CC anchored PCR technique was employed to isolate CD30-L human and murine  
CC clones containing an additional 19 N-terminal amino acid sequence  
CC (AAQ53537, AAQ53538).

XX Sequence 720 BP; 191 A; 196 C; 161 G; 172 T; 0 other;

Query Match 99.8%; Score 661.4; DB 14; Length 720;  
Best Local Similarity 99.8%; Pred. No. 1.1e-199;  
Matches 662; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ATGAGGTGCGAGCCCGCTGGTACGAGCCCTGGAGAACGACGAGCCCTGGAGAAGC 60

Db 58 atgcaggtgcagcccggtcgtgtagccagccctggagaagcacgagccctggagaagc 117

QY 61 ACAAGTCGACGACTTCTACCTCAGCACACCGCAGCTGGTGTGCTTGTGTGGCAGTG 120

Db 118 acaagtgcagctacttctacctcagcaccaccgactggtgtgcttgtgtgctgagtg 177

QY 121 GCGATCATCTGGTACGTGGTAGTCCAGAAAAGGACTCCACTCCAAATACAACTGAGAAG 180

Db 178 gcgatcattcgtgactggtgtagtcagaaaaaggactccactccaaatacaactgagaag 237

QY 181 GCCCCCTTAAAGGAGGAATTTGCTCAGAGGATCTCTCTGCTACCTGAAAAGTACTCCA 240

Db 238 gccccccttaagaggaaattgtcagaggatctcttctgtaccctgaaagtaactcca 297

QY 241 TCCAAGAAGTCATGGGCTACCTCCAAAGTGTCAAAAGCATCTCAACAATACCAAACTGTCA 300  
Db 298 tccaagaagtcattgggctacctccaagtgtcaaaagcatctcaacaataccaaactgtca 357  
QY 301 TGAACGCAAGATGCGACCATCCAGGACTCATATACAGGACGCGGAACTGTATAGTCCAA 360  
Db 358 tggaaaggaagatggcaccatccacggactcatataccagagcagggaaacctgagatccaa 417  
QY 361 TTCCCTGGCTTGTACTTTCATCGTTTGCCAACTGCAGTTCCTCGTGCAGTGTCTCAAAATCAT 420  
Db 418 ttccctggcttgaacttcacgttggccaactgcagttcctctgcagtgctcaaatcat 477  
QY 421 TCTGTGGAACATGACATTCGAGTCCCTCATCAATTCCAAGATCAAAAAGCAGACGTTGGTA 480  
Db 478 tctgtggaacctgacattgcagctcctcatcaattccaagatcaaaaagcagagtggtga 537  
QY 481 ACAGTGTGAGTCTGGAGTTGAGAGTAAGAACATCTACCAGATCTCTCTCAGTTTGTG 540  
Db 538 acagtgtgtgagtcgtgagttcagagtaagaacatctaccagaaatctctctcagttttg 597  
QY 541 CTGCATTACTTACAGGTCAACTCTACCATATCAGTCAAGGTGGGATAATTTCCAGTATGTG 600  
Db 598 ctgcattactacaggtcaactctaccatcatcagtcagtgaggtcaggtatccagtgatctg 657  
QY 601 GATACAAACACTTTCCCTCTTGATAATGTGCTATCCGCTCTTCTATATAGTAGTACAGAC 660  
Db 658 gatacaaacactttccctcttgataatgtgctatcgtatcgttcttattatagtagctcagac 717  
QY 661 TGA 663  
Db 718 tga 720

RESULT 5

AAQ53536  
ID AAQ53536 standard; cDNA; 648 BP.

XX AC AAQ53536;

XX DT 19-JUN-1994 (first entry)

XX Sequence of the coding region of a human CD30-L cDNA clone.

DE Hodgkin's disease; lymphoma; surface antigen; cytokine;

KW CD30 ligand; CD30-L; TNF; NGF; ss.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT CDS 1..648

FT /\*tag= a

XX WO9324135-A.

XX 09-DEC-1993.

XX 25-MAY-1993; 93WO-US04926.

XX 26-MAY-1992; 92US-0889717.

XX 02-JUN-1992; 92US-0892459.

XX 15-JUN-1992; 92US-0899660.

XX 01-JUL-1992; 92US-0907224.

XX 27-OCT-1992; 92US-0966775.

XX (IMMV ) IMMUNEX CORP.

XX Armitage RJ, Goodwin RG, Smith CA;

XX WPI; 1993-405417/50.

XX P-PSDB; AAR45007.

XX New cytokine, CD30-L, which binds CD30 - used for developing  
PT prods. for diagnosis, detection, purifications, research and





Db 263 gcatcgtgaaagagctccatcaagaagtcattggtccctccacccagtggaagcattc 322  
Qy 281 TCAACAATACCAAACTGTCATGGAAGAGATGCGACCATCCACGGAGTCTATACACAGG 340  
Db 323 taacaaacacacagtggtcttggaacaaagatggcattcccatggagtcagatcag 382  
Qy 341 ACGGGAACCTGATAGTCCCAATTCCTCGGCTGTGACTTCATCGTTTGCACACTGCAGTCC 400  
Db 383 atgggaatctggtgattcccaattccctgggttgtaactcatcatttgccaactgcagttc 442  
Qy 401 TCGTCAGTGTCAAAATCAATTCGTGGACCTGACATTCGACGTCCTCATCAATTCACAAGA 460  
Db 443 ttgtacaatgcccaataattctgtogactctgaagtggagctctctcaacaagcata 502  
Qy 461 TCAAAAAGCAGACGTGGTAACAGTGTGTGACGTCGTGGAGTTCAGAGTAAGAATCTTACC 520  
Db 503 tcaaaaacacagccctggtagcagtgtgtgactggaatgcaacgaaacagataacc 562  
Qy 521 AGAATCTCTCTCAGTGTGTCATTAATTCAGTCACTTACAGTCACTTACATATCATGTCAGGG 580  
Db 563 agaattctctcaattctgtgattacctgcaggtcaacacaccataatcagtaagt 622  
Qy 581 TGGATAATTCAGATGTGGATACAAACACTTCCCTCTTGTGATAATGTGCTATCCGCTCT 640  
Db 623 tggatacatccagtcacatagatacaagcacctttctctctgtgagaatgtgtgtccatct 682  
Qy 641 TCTTATATAGTAGTCAAGACTCA 663  
Db 683 tcttatacagtaattccagactga 705

## RESULT 7

AAV39012 standard; DNÀ; 1906 BP.

XX AAV39012;

AC AAV39012;

XX 23-SEP-1998 (first entry)

XX CD30 ligand gene used in the course of the invention.

XX Human; CD30 ligand; alteration; immunoreactivity; human cell;

KW accessory molecule ligand; AML; gene therapy; treatment; neoplasia;

KW autoimmune disorder; rheumatoid arthritis; vaccine; ss.

XX Homo sapiens.

XX MO9826061-A2.

XX 18-JUN-1998.

XX 08-DEC-1997; 97WO-US22740.

XX 01-DEC-1997; 97US-0982272.

PR 09-DEC-1996; 96US-0032145.

XX (REGC ) UNIV CALIFORNIA.

XX Cantwell M, Kipps TJ, Sharma S;

XX WPI; 1998-348521/30.

XX Vectors containing accessory molecule ligand genes - used for

PT altering immunoreactivity of cells, particularly for treatment of

PT neoplasia or autoimmune disorders, e.g. rheumatoid arthritis

XX Disclosure; Page 114; 167pp; English.

XX The present sequence represents a CD30 ligand gene. The sequence is

CC used to exemplify the method of the invention. The specification

CC describes a method for altering the immunoreactivity of human cells

CC which comprises introducing a gene encoding an accessory molecule

CC ligand (AML) into the cells so that the AML is expressed on the surface  
CC of the cells. Vectors containing the AML genes can be used in gene  
CC therapy for treating neoplasia or autoimmune disorders such as rheumatoid  
CC arthritis. They can also be used for vaccination to produce immunity  
CC against a virus cell, bacteria, protein, fungus or neoplasia.  
XX  
SQ Sequence 1906 BP; 559 A; 447 C; 438 G; 462 T; 0 other;

Query Match 60.7%; Score 402.2; DB 19; Length 1906;

Best Local Similarity 79.0%; Pred. No. 2.9e-117;

Matches 492; Conservative 0; Mismatches 128; Indels 3; Gaps 1;

Qy 44 CGAGGCCCTGAGAGACAAAGTCGACGCTACTTCTACTCTCAGCACCCACGCACTGG--- 100  
Db 197 ccagccacctgggacacacagcgcgcagctattctattgaccacacccactctggctc 256

Qy 101 TGTCCCTTGTGTGGCAGTGGCGATCATTTCTGTACTGTGTAGTCCAGAAAAGGACTCCA 160  
Db 257 tgtcccttgttccagcgtggccactattatgtgtgtgttcagagcgagactcca 316

Qy 161 CTCCAATATACAACTGAGNAGGCCCCCTTAAAGGAGGAAATGCTCAGAGGATCTCTTCT 220  
Db 317 ttcccaactcaactgacaacgtcccccctcaagaggagaaattgtctcagaagacctcttat 376

Qy 221 GTACCCCTGAAAGTACTCCATCCAAAGAGTCAATGGGCCCTACTCTCAAGTGTCAAAGCATC 280  
Db 377 gtaccttgaaagagctccattccaagaagtcattgggcccactccaagtggcaagcactc 436

Qy 281 TCAACAATACCAAACTGTCTATGSAACGAAGATGCCACCATCCACGGACTCATATACCAGG 340  
Db 437 taacaaacacacagtggtcttggaacaaagatggcattctccatggagtcagatcagg 496

Qy 341 ACGGGAACCTGATAGTCCCAATTCCTCGCTTGTACTTCAATCGTTTGCACACTGCAGTTC 400  
Db 497 atgggaatctggtgatcccaattccctggtgtgtactcatcttggcaactgcagtttc 556

Qy 401 TCGTCAGTGTCTCAAAATCATTTCTGTGGACCTGCATTTGCAGCTCTCTCATCAATTCACA 460  
Db 557 ttgtacaatgcccaataattctgtcagatctgaagttggagcttctcacaacagcata 616

Qy 461 TCAAAAAGCAGACGCTGTGTGAACAGTGTGTAGTCTGGAGTTCAGAGTAAGAACAATCTACC 520  
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Qy 521 AGAATCTCTCTCAGTGTGCTGCTGCTACTTACTTACAGGTCAACTCTACCATATCAGTCAGG 580  
Db 677 agaattctctcaattctgtggttaccctgcaggtgcaacacaccacataatcagtcagt 736

Qy 581 TGGATAATTTCCAGTATGTGGATACAAACACTTTCCTCTTGTGATAATGTGTCATCCGCTCT 640  
Db 737 tggatacatccagtcacatagatacaagcacccttctctctgtgagaatgtgtgtccatct 796

Qy 641 TCTTATATAGTACTCAGACTGA 663  
Db 797 tcttatacagtaattccagactga 819

## RESULT 8

AAF58252

ID AAF58252 standard; DNA; 936 BP.

XX AC

XX AAF58252;

XX AC

XX 24-APR-2001 (first entry)

XX DE

XX Oligonucleotide D1835.

XX XX

KW Electron-transfer group; ETM; mismatch; genotyping;

XX gene expression; ss.

XX Synthetic.

XX XX

```

PN XX WO200107665-A2.
XX PD 01-FEB-2001.
XX PF 26-JUL-2000; 2000WO-US20476.
XX PR 26-JUL-1999; 99US-0145695.
XX PR 17-MAR-2000; 2000US-0190259.
XX PA (CLIN-) CLINICAL MICRO SENSORS INC.
XX PI Umek RM;
XX DR WPI; 2001-159728/16.
XX CC Nucleic acids containing electron-transfer group, useful as labels in
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
PT a single surface -
XX PS Example 6; Page 127; 159pp; English.
XX CC The present invention relates to a composition comprising two nucleic
CC acids each containing an electron-transfer group (ETM) having
CC different redox potentials. The invention is used for electronic
CC detection of nucleic acids, especially of substitutions (mismatches)
CC and single-nucleotide polymorphisms, e.g. for genotyping,
CC monitoring gene expression.
XX CC Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;
SQ

Query Match 6.4%; Score 42.6; DB 22; Length 936;
Best Local Similarity 1.3%; Pred. NO. 0.002;
Matches 6; Conservative 260; Mismatches 199; Indels 0; Gaps

QY 188 TTAAGGAGGAATTCCTCAGAGGATCTCTCTGTACCTGAAAGTACTCCATCCAGA 247
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
40 www.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwcw 99

QY 248 AGTCATGGCCCTACCTCCAAGTGTCAAAGCATCTCAACAATACCAACTGTCATGGAACG 307
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
100 www.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwww 159

QY 308 AAGATGGCACCATCCAGCGACTCATATACAGGACGGGAACCTGATGCCAATTCCTCG 367
Db : : : : : : : : : : : : : : : : | : : : : : : : : : :
160 www.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwww 219

QY 368 GCTTGTTACTTCATCGTTGCCAACTGCAGTTCCTCTGTGAGTGCTCAAATCATCTGTGG 427
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
220 www.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwww 279

QY 428 ACCTGACATTGCAGCTCCCTCATCAATCCAAAGATCAAAGACGAGCTTGTTAACAGTGT 487
Db : : : : : | : : : : : : : : : : : : : : : : : : : : : :
280 www.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwww 339

QY 488 GTGAGTCGGAGTTCCAGAGTAAGAACATCTACAGAAATCTCTCAGTTTTTGTGCTGCATT 547
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
340 www.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwww 399

QY 548 ACTTACAGTCAACTCTACCATATCAGTCAGGGTGGATAATTTCCAGTATGTGGATACAA 607
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
400 www.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwww 459

QY 608 ACACATTCCTCCTTGATATGTGCTATCGCTCTCTTATATAGTA 652
Db : : : : : : : : : : : : : : : : | : : : : : : : : : :
460 www.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwwww.wwww 504

RESULT 9
AAF58252/C
ID AAF58252 standard; DNA; 936 BP..
XX AC
AAF58252;
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[illegible]

Query Match 6.4%; Score 42.6; DB 22; Length 936;  
Best Local Similarity 1.1%; Pred. No. 0.002;  
Matches 6: Conservative 202; Mismatches 231; Indels 0; Gaps 0.

RESULT	9
AAF58252/C	
ID	AAF58
XX	
AC	AAF58

[illegible]



PT Nucleic acids containing electron-transfer group, useful as labels in  
PT hybridization assays, e.g. for genotyping, allowing repeat analyses on  
PT a single surface  
XX  
XX  
PS Example 6; Page 127; 159pp; English.  
XX  
CC The present invention relates to a composition comprising two nucleic  
CC acids each containing an electron-transfer group (ETM) having  
CC different redox potentials. The invention is used for electronic  
CC detection of nucleic acids, especially of substitutions (mismatches)  
CC and single-nucleotide polymorphisms, e.g. for genotyping,  
CC monitoring gene expression.  
XX  
SQ Sequence 936 BP; 5 A; 142 C; 7 G; 6 T; 776 other;

[illegible]

RESULT	14
AAF58259	
ID	AAF58259 standard; DNA; 936 BP.
XX	
XX	AAF58259;
XX	
XX	
DT	24-APR-2001 (first entry)
XX	
DE	Oligonucleotide D2004.

Electron-transfer group; ETM; mismatch; genotyping;	XX
gene expression; ss.	XX
Synthetic.	OS
	XX
WO200107665-A2.	PN

XX PD XX PF XX PR PR XX PA XX PI XX DR XX PT PT PT XX PS XX CC CC CC CC CC CC XX SQ

Query Match 6.4%; Score 42.6; DB 22; Length 936;  
Best Local Similarity 1.3%; Pred. NO. 0.002;  
Matches 6; Conservative 260; Mismatches 199; Indels 0; Gaps 0;

[illegible]

RESULT 15  
AAF58259/C  
ID AAF58259 standard; DNA; 936 BP.  
XX  
XX AAF58259;  
XX



GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 5, 2001, 21:50:21 ; Search time 1465.36 Seconds  
(without alignments)  
6998.361 Million cell updates/sec

Title: US-09-628-126-18  
Perfect score: 663  
Sequence: 1 ATCGAGTGGAGCCCGGCTC.....TATATAGTACTGACTGA 663

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1344157 seqs, 7733874588 residues

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: gb\_ba3.\*  
4: gb\_in1.\*  
5: gb\_in2.\*  
6: gb\_in3.\*  
7: gb\_om.\*  
8: gb\_ov.\*  
9: gb\_pat1.\*  
10: gb\_pat2.\*  
11: gb\_ph.\*  
12: gb\_pl1.\*  
13: gb\_pl2.\*  
14: gb\_pl3.\*  
15: gb\_pl4.\*  
16: em\_ba1.\*  
17: em\_ba2.\*  
18: em\_fun.\*  
19: em\_htgo\_hum.\*  
20: em\_htgo\_inv.\*  
21: em\_htgo\_rod.\*  
22: em\_htg\_hum1.\*  
23: em\_htg\_hum2.\*  
24: em\_htg\_hum3.\*  
25: em\_htg\_hum4.\*  
26: em\_htg\_hum5.\*  
27: em\_htg\_hum6.\*  
28: em\_htg\_hum7.\*  
29: em\_htg\_hum8.\*  
30: em\_htg\_inv1.\*  
31: em\_htg\_inv2.\*  
32: em\_htg\_other.\*  
33: em\_htg\_rod.\*  
34: em\_hum1.\*  
35: em\_hum2.\*  
36: em\_hum3.\*  
37: em\_hum4.\*  
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40: em\_hum7.\*  
41: em\_in.\*  
42: em\_om.\*  
43: em\_or.\*

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45: em\_pat.\*  
46: em\_ph.\*  
47: em\_pl.\*  
48: em\_ro.\*  
49: em\_sts.\*  
50: em\_sy.\*  
51: em\_un.\*  
52: em\_vi.\*  
53: gb\_sts1.\*  
54: gb\_sts2.\*  
55: gb\_sts3.\*  
56: gb\_sy.\*  
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96: gb\_in4.\*  
97: gb\_pr10.\*  
98: em\_ba3.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	663	100.0	663	9 AR007977	AR007977 Sequence
2	663	100.0	663	10 I16911	I16911 Sequence 18
3	663	100.0	663	10 I69504	I69504 Sequence 18
4	663	100.0	720	9 AR007968	AR007968 Sequence
5	663	100.0	720	10 I16902	I16902 Sequence 5
6	663	100.0	720	10 I69495	I69495 Sequence 5
7	663	100.0	1783	94 MUSCD30	L09754 Mus musculus
8	402.2	60.7	648	9 AR007978	AR007978 Sequence



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9 402.2 60.7 648 10 I16912 Sequence 22
10 402.2 60.7 648 10 I69505 Sequence 22
11 402.2 60.7 705 9 AR007969 Sequence 7
12 402.2 60.7 705 10 I16903 Sequence 7
13 402.2 60.7 705 10 I69496 Sequence 7
14 402.2 60.7 1906 97 HUMCD30 L09753 Homo sapien
15 313.4 47.3 660 56 AF081364 AF081364 Synthetic
16 275 41.5 158717 89 AL133412 AL133412 Human DNA
17 272.2 41.1 1313 93 HSCD30L4 AF006384 Homo sapi
18 62.8 9.5 807 93 HSCD30L3 AF006383 Homo sapi
19 42 6.3 2859 93 HSCD30L1 AF006381 Homo sapi
20 41.8 6.3 155065 93 HSU659119 AL122003 Human DNA
21 41.6 6.3 145415 93 HSB4388K2 AL121584 Human DNA
22 40.6 6.1 35802 6 CEF58A3 Z81017 Caenorhabdi
23 40.6 6.1 172135 75 AC074009 AC074009 Homo sapi
24 40.6 6.1 183561 62 AC012452 AC012452 Homo sapi
25 40.6 6.1 187013 72 AC055842 AC055842 Homo sapi
26 40.6 6.1 187277 76 AC079803 AC079803 Homo sapi
27 40.4 6.1 1054 15 U01103 U01103 Arabidopsis
28 40.4 6.1 84432 12 AC005850 AC005850 Arabidops
29 40.2 6.1 160012 68 AC024109 AC024109 Homo sapi
30 40.2 6.1 161822 70 AC026306 AC026306 Homo sapi
31 37.4 5.6 1740 6 CEU80221 U80221 Caenorhabdi
32 37.4 5.6 1779 6 CEU80220 U80220 Caenorhabdi
33 37.4 5.6 12249 1 AE006545 AE006545 Streptoco
34 37.2 5.6 114847 92 HS257120 AL021878 Human DNA
35 37.2 5.6 199814 6 CEY4703A AL117202 Caenorhab
36 37.2 5.6 337565 83 CEV47D3 Z98865 Caenorhabdi
37 36.4 5.5 95751 71 AC044832 AC044832 Homo sapi
38 36.4 5.5 148270 70 AC027579 AC027579 Homo sapi
39 36.4 5.5 174405 67 AC022727 AC022727 Homo sapi
40 36.4 5.5 179792 82 AP001531 AP001531 Homo sapi
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42 36.2 5.5 184635 69 AC025827 AC025827 Homo sapi
43 36.2 5.5 225559 76 AC084042 AC084042 Mus muscu
44 36 5.4 198872 89 AF297093 AF297093 Homo sapi
45 35.8 5.4 1710 5 AF027123 AF027123 Drosophil
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## ALIGNMENTS

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RESULT 1
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LOCUS AR007977 663 bp DNA PAT 04-DEC-1998
DEFINITION Sequence 18 from patent US 5753203.
ACCESSION AR007977
VERSION AR007977.1 GI:3967086
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 663)
AUTHORS Goodwin,R.G., Smith,C.A., Armitage,R.J. and Gruss,H.
TITLE CD30 ligand conjugates
JOURNAL Patent: US 5753203-A 18 19-MAY-1998;
FEATURES
Location/Qualifiers
source 1. 663
BASE COUNT 180 a 175 c 144 g 164 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 8.1e-189;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ATGCAGGTGCAGCCGGCTCGGTAGCCAGCCCTGGAGAGCAGCAGGCCCTGGAGAAGC 60
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Qy 61 ACAAGTCCAGCTACTTCTTACCTCAGCACCACCGCACTGGTGTGCTTGTGTGGCAGTG 120
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Query Match 100.0%; Score 663; DB 10; Length 663;
Best Local Similarity 100.0%; Pred. No. 8.1e-189;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCAGGTGCAGCCGGCTCGGTAGCCAGCCCTGGAGAGCAGCAGGCCCTGGAGAAGC 60
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Qy 61 ACAAGTCCAGCTACTTCTTACCTCAGCACCACCGCACTGGTGTGCTTGTGTGGCAGTG 120
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LOCUS 169504 663 bp DNA PAT 04-FEB-1998
DEFINITION Sequence 18 from patent US 5677430.
ACCESSION 169504
VERSION 169504.1 GI:2831626
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 663)
AUTHORS Goodwin,R.G., Smith,C.A., Armitage,R.J. and Gruss,H.
TITLE Antibodies directed against CD30 ligand
JOURNAL Patent: US 5677430-A 18 14-OCT-1997;
FEATURES Location/Qualifiers
source 1..663
/organism="unknown"
BASE COUNT 180 a 175 c 144 g 164 t
ORIGIN
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Query Match 100.0%; Score 663; DB 10; Length 663;  
Best Local Similarity 100.0%; Pred. No. 8.1e-189;  
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 ATGCAGGTGCACCCGGCTCGGTAGCCAGCCCTCGAGAGCAGCAGGCCCTGGAGAGC 60
Db 1 ATGCAGGTGCACCCGGCTCGGTAGCCAGCCCTCGAGAGCAGCAGGCCCTGGAGAGC 60
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Qy 61 ACAAGTCGAGCTACTTCTACCTCAGCACCCAGCGACTGGTGTGCTGTGTTGGCAGTG 120
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Db 361 TTCCTTGGCTTGTACTTCACTGTTTCCCAACTGCAGTTCCTCTGAGTGCCTCAAAATCAT 420
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Qy 661 TGA 663
Db 661 TGA 663
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RESULT 4
AR007968
LOCUS AR007968 720 bp DNA PAT 04-DEC-1998
DEFINITION Sequence 5 from patent US 5753203.
ACCESSION AR007968
VERSION AR007968.1 GI:3967077
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 720)
AUTHORS Goodwin,R.G., Smith,C.A., Armitage,R.J. and Gruss,H.
TITLE CD30 ligand conjugates
JOURNAL Patent: US 5753203-A 5 19-MAY-1998;
FEATURES Location/Qualifiers
source 1..720
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BASE COUNT 191 a 195 c 162 g 172 t
ORIGIN
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Query Match 100.0%; Score 663; DB 9; Length 720;  
Best Local Similarity 100.0%; Pred. No. 8.2e-189;  
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 ACAAGTCGACGCTACTTCTACCTCAGCACACCGCAGCTGGTGGCTTGTGTGGCAGTG 120
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Db 118 ACAAGTCGACGCTACTTCTACCTCAGCACACCGCAGCTGGTGGCTTGTGTGGCAGTG 177
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Db 178 GCGATCATCTCGGCTAGTCCAGAAAAGGACTCCACTCCAAATACAACTGAGAAG 237
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QY 361 TTCCCTGGCTGTACTTCATCGTTTGCCAACTGCAGTTCCTCGTGCAGTCTCAATCAT 420
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Db 478 TCTGTGGACCTGCAGTTCAGCTCCTCATCAATTCGAAGATCAAAAGCAGACGTTGGTA 537
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QY 481 ACAGTGTGTAGTCTGGAGTTTCAGAGTGAAGACATCTACCAAGATCTCTCTCAGTTTTG 540
Db 538 ACAGTGTGTAGTCTGGAGTTTCAGAGTGAAGACATCTACCAAGATCTCTCTCAGTTTTG 597
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QY 541 CTGCATTACTTACAGGTCACCTTACCATATCAGTCAGGTTGGATAATTTCCAGTATGTG 600
Db 598 CTGCATTACTTACAGGTCACCTTACCATATCAGTCAGGTTGGATAATTTCCAGTATGTG 657
|||||
QY 601 GATACAAACACTTTCCCTCTTGATAATGCTATCCGCTCTCTTATATAGTAGTACGAC 660
Db 658 GATACAAACACTTTCCCTCTTGATAATGCTATCCGCTCTCTTATATAGTAGTACGAC 717
|||||
QY 661 TGA 663
|||
Db 718 TGA 720

RESULT 5
LOCUS 116902 720 bp DNA PAT 03-APR-1996
DEFINITION Sequence 5 from patent US 5480981.
ACCESSION 116902
VERSION 116902.1 GI:1251810
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1. (bases 1 to 720)
AUTHORS Goodwin,R.G., Smith,C.A., Armitage,R.J. and Gruss,H.
TITLE CD30 ligand
JOURNAL Patent: US 5480981-A 5 02-JAN-1996;
FEATURES Location/Qualifiers
source 1..720
BASE COUNT 191 a 195 c 162 g 172 t
ORIGIN

Query Match 100.0%; Score 663; DB 10; Length 720;
Best Local Similarity 100.0%; Pred. No. 8.2e-189;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCAGTGCAGCCGCTCGGTAGCCAGCCCTGGAGAAGCAGGCGCTGGAGAAGC 60
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Db 58 ATGCAGTGCAGCCGCTCGGTAGCCAGCCCTGGAGAAGCAGGCGCTGGAGAAGC 117
QY 61 ACAAGTCGACGCTACTTCTACCTCAGCACACCGCAGCTGGTGGCTTGTGTGGCAGTG 120
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Db 118 ACAAGTCGACGCTACTTCTACCTCAGCACACCGCAGCTGGTGGCTTGTGTGGCAGTG 177
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QY 121 GCGATCATCTCGGCTAGTCCAGAAAAGGACTCCACTCCAAATACAACTGAGAAG 180
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Db 178 GCGATCATCTCGGCTAGTCCAGAAAAGGACTCCACTCCAAATACAACTGAGAAG 237
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QY 181 GCCCCCTTAAAGGAGGAAATGCTCAGAGGATCTTCTGTACCTGAAAAGTACTCCA 240
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Db 238 GCCCCCTTAAAGGAGGAAATGCTCAGAGGATCTTCTGTACCTGAAAAGTACTCCA 297
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QY 241 TCCAAGAGTCAATGGGCTTACCTCCAAAGTGTCAAAAGCATCTCAAAATACCAAACTGTCA 300
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Db 298 TCCAAGAGTCAATGGGCTTACCTCCAAAGTGTCAAAAGCATCTCAAAATACCAAACTGTCA 357
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QY 301 TGGAAAGAGTGGACCATCCAGGACTCATATACAGGAGGGAACCTGATAGTCCAA 360
Db 358 TGGAAAGAGTGGACCATCCAGGACTCATATACAGGAGGGAACCTGATAGTCCAA 417
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QY 361 TTCCCTGGCTGTACTTCATCGTTTGCCAACTGCAGTTCCTCGTGCAGTCTCAATCAT 420
Db 418 TTCCCTGGCTGTACTTCATCGTTTGCCAACTGCAGTTCCTCGTGCAGTCTCAATCAT 477
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QY 421 TCTGTGGACCTGCAGTTCAGCTCCTCATCAATTCGAAGATCAAAAGCAGACGTTGGTA 480
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QY 481 ACAGTGTGTAGTCTGGAGTTTCAGAGTGAAGACATCTACCAAGATCTCTCTCAGTTTTG 540
Db 538 ACAGTGTGTAGTCTGGAGTTTCAGAGTGAAGACATCTACCAAGATCTCTCTCAGTTTTG 597
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QY 541 CTGCATTACTTACAGGTCACCTTACCATATCAGTCAGGTTGGATAATTTCCAGTATGTG 600
Db 598 CTGCATTACTTACAGGTCACCTTACCATATCAGTCAGGTTGGATAATTTCCAGTATGTG 657
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QY 601 GATACAAACACTTTCCCTCTTGATAATGCTATCCGCTCTCTTATATAGTAGTACGAC 660
Db 658 GATACAAACACTTTCCCTCTTGATAATGCTATCCGCTCTCTTATATAGTAGTACGAC 717
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QY 661 TGA 663
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Db 718 TGA 720

RESULT 6
LOCUS 169495 720 bp DNA PAT 04-FEB-1998
DEFINITION Sequence 5 from patent US 5677430.
ACCESSION 169495
VERSION 169495.1 GI:2831617
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 720)
AUTHORS Goodwin,R.G., Smith,C.A., Armitage,R.J. and Gruss,H.
TITLE Antibodies directed against CD30 ligand
JOURNAL Patent: US 5677430-A 5 14-OCT-1997;
FEATURES Location/Qualifiers
source 1..720
BASE COUNT 191 a 195 c 162 g 172 t
ORIGIN

Query Match 100.0%; Score 663; DB 10; Length 720;
Best Local Similarity 100.0%; Pred. No. 8.2e-189;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGCAGTGCAGCCGCTCGGTAGCCAGCCCTGGAGAAGCAGGCGCTGGAGAAGC 60
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Db 58 ATGCAGGTGCACCCGGCTCGTAGCCAGCCCTGGAGAAGCAGAGGCCCTGGAGAAGC 117
Qy 61 ACAAGTCGACGACTACTTCTACCTCAGCACCACCGCAGCTGGTGGCTTGTGTGGCAGTG 120
Db 118 ACAAGTCGACGACTACTTCTACCTCAGCACCACCGCAGCTGGTGGCTTGTGTGGCAGTG 177
Qy 121 GCGATCATCTCGTACTGGTAGTCCAGAAAAAGGACTCCACTCCAATACAACTGAGAAG 180
Db 178 GCGATCATCTCGTACTGGTAGTCCAGAAAAAGGACTCCACTCCAATACAACTGAGAAG 237
Qy 181 GCCCCCTTAAAGGAGGAATGCTCAGAGGATCTCTGTGTACCTCGAAAGTACTCCA 240
Db 238 GCCCCCTTAAAGGAGGAATGCTCAGAGGATCTCTGTGTACCTCGAAAGTACTCCA 297
Qy 241 TCCAAAGAGTCATGGCCCTACCTCCAAGTGTCAAAAGCATCTCAACAATACCAAACTGTCA 300
Db 298 TCCAAAGAGTCATGGCCCTACCTCCAAGTGTCAAAAGCATCTCAACAATACCAAACTGTCA 357
Qy 301 TGGACGAGATGGACACATCCACGACTCATATACAGAGCGGGAACCTGATAGTCCAA 360
Db 358 TGGAAAGAGATGGACACATCCACGACTCATATACAGAGCGGGAACCTGATAGTCCAA 417
Qy 361 TTCCTCGCTTCTACTTCTATCTGTCGCAACTGCAGTCTCTGTGAGTGCCTCAAAATCAT 420
Db 418 TTCCTCGCTTCTACTTCTATCTGTCGCAACTGCAGTCTCTGTGAGTGCCTCAAAATCAT 477
Qy 421 TCTGTGGACCTGACATTTGAGCTTCTCATCAATTCGAAGATCAAAAGCAGAGCTTGGTA 480
Db 478 TCTGTGGACCTGACATTTGAGCTTCTCATCAATTCGAAGATCAAAAGCAGAGCTTGGTA 537
Qy 481 ACAGTGTGAGTCTGGAGTTCAGAGTAGAGACATCTACAGAAATCTCTCTCAGTTTTGG 540
Db 538 ACAGTGTGAGTCTGGAGTTCAGAGTAGAGACATCTACAGAAATCTCTCTCAGTTTTGG 597
Qy 541 CTGCATTACTTACAGTCAACTCTACCATATCAGTCAAGTGGTATATTCAGTATGTG 600
Db 598 CTGCATTACTTACAGTCAACTCTACCATATCAGTCAAGTGGTATATTCAGTATGTG 657
Qy 601 GATCAAAACACTTTCCCTCTTGATATGTGCTATCGCTCTCTTATATAGTACTCAGAC 660
Db 658 GATCAAAACACTTTCCCTCTTGATATGTGCTATCGCTCTCTTATATAGTACTCAGAC 717
Qy 661 TGA 663
Db 718 TGA 720

RESULT 7
MUSCD30 1783 bp mRNA ROD 23-AUG-1995
LOCUS Mus musculus Cd30 ligand mRNA, complete cds.
DEFINITION L09754
ACCESSION L09754
VERSION L09754.1 GI:349288
KEYWORDS CD30 ligand; transmembrane protein type II.
SOURCE Mus musculus cdna to mRNA.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1783)
AUTHORS Smith,C.A., Gruss,H.J., Davis,T., Anderson,D., Farrah,T., Baker,E.,
Sutherland,G.R., Brannan,C.I., Copeland,N.G., Jenkins,N.A.,
Grabstein,K.H., Gliniak,B., McAllister,I.B., Fanslow,W.,
Alderson,M., Falk,B., Gimpel,S., Gillis,S., Din,W.S., Goodwin, R.G.
and Armitage,R.J.
TITLE CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
ligand defines an emerging family of cytokines with homology to TNF
JOURNAL Cell 73 (7), 1349-1360 (1993)
MEDLINE 93313964
FEATURES Location/Qualifiers
source
1..1783
/organism="Mus musculus"
/db_xref="taxon:10090"

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/cell_line="789"
/cell_type="r-cell"
113..832
/notes="homology to TNF and ligand CD40; potential
glycosylation sites (75,86,114,158,174,186)"
/codon_start=1
/product="CD30 antigen"
/protein_id="AA74595.1"
/db_xref="GI:349288"
/translaton="MEFLOAGSCGAPSDPMQVQPSVAPWRSRSTSRYS
FYLSSTALVCLVVAAILLVVQKKDSTPNTTEKAPKGGNGSEDLFLKSTPSKK
SWAYLOVSKHLNKLNSWEDGTIHGLIYVDGNLIYVQPLGYFTVCOLOFLVOCNSHS
VDLTQLLINSKIKKOTLVTVCSGVQSKNIYQNLQFLHLHYLVNSTISVRVDFQY
VDNTFPDLNVLVSFLVSSD"
BASE COUNT 515 a 411 c 407 g 450 t
ORIGIN

Query Match 100.0%; Score 663; DB 94; Length 1783;
Best Local Similarity 100.0%; Pred. No. 9.2e-189;
Matches 663; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCAGGTGCAGCCGGCTCGTAGCCAGCCCTGGAGAAGCAGAGGCCCTGGAGAAGC 60
Db 170 ATGCAGGTGCAGCCGGCTCGTAGCCAGCCCTGGAGAAGCAGAGGCCCTGGAGAAGC 229
Qy 61 ACAAGTCGACGACTACTTCTACCTCAGCACCACCGCAGTGGTGTGCTTGTGTGGCAGTG 120
Db 230 ACAAGTCGACGACTACTTCTACCTCAGCACCACCGCAGTGGTGTGCTTGTGTGGCAGTG 289
Qy 121 GCGATCATCTCGTACTGGTAGTCCAGAAAAAGGACTCCACTCCAATACAACTGAGAAG 180
Db 290 GCGATCATCTCGTACTGGTAGTCCAGAAAAAGGACTCCACTCCAATACAACTGAGAAG 349
Qy 181 GCCCCCTTAAAGGAGGAATTTGCTCAGAGATCTCTTCTGTACCTCGAAAGTACTCCA 240
Db 350 GCCCCCTTAAAGGAGGAATTTGCTCAGAGATCTCTTCTGTACCTCGAAAGTACTCCA 409
Qy 241 TCCAAAGATCATGGGCTTACCTCCAAGTGTCAAAAGCATCTCAACAATACCAAACTGTCA 300
Db 410 TCCAAAGATCATGGGCTTACCTCCAAGTGTCAAAAGCATCTCAACAATACCAAACTGTCA 469
Qy 301 TGGAAAGAGATGGACCATCCAGGACTCATATACAGAGGAGGGAACTCGATAGTCCAA 360
Db 470 TGGAAAGAGATGGACCATCCAGGACTCATATACAGAGGAGGGAACTCGATAGTCCAA 529
Qy 361 TTCCTCGCTTGTACTTTCATCGTTTGGCAACTGCAGTTCCTCGTGCAGTCTCAAAATCAT 420
Db 530 TTCCTCGCTTGTACTTTCATCGTTTGGCAACTGCAGTTCCTCGTGCAGTCTCAAAATCAT 589
Qy 421 TCTGTGGACCTGACATTTGCGAGTCTCTCATCAATTTCCAAGATCAAAAAGCAGACGTTGGTA 480
Db 590 TCTGTGGACCTGACATTTGCGAGTCTCTCATCAATTTCCAAGATCAAAAAGCAGACGTTGGTA 649
Qy 481 ACAGTGTGAGTCTGGAGTTCAGAGTAGAAGCAATCTACCAAGATCTCTCTCAGTTTTGG 540
Db 650 ACAGTGTGAGTCTGGAGTTCAGAGTAGAAGCAATCTACCAAGATCTCTCTCAGTTTTGG 709
Qy 541 CTGCATTACTTACAGTCAACTCTACCATATCAGTCAAGGTTGGATATTTCCAGTATGTG 600
Db 710 CTGCATTACTTACAGTCAACTCTACCATATCAGTCAAGGTTGGATATTTCCAGTATGTG 769
Qy 601 GATCAAAACACTTTCCCTCTTGATATGTGTATATCCGCTCTCTTATATAGTAGTCTCAGAC 660
Db 770 GATCAAAACACTTTCCCTCTTGATATGTGTATATCCGCTCTCTTATATAGTAGTCTCAGAC 829
Qy 661 TGA 663
Db 830 TGA 832

RESULT 8
AR007978

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LOCUS AR007978 648 bp DNA PAT 04-DEC-1998  
DEFINITION Sequence 22 from patent US 5753203.  
ACCESSION AR007978  
VERSION AR007978.1 GI:3967087  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 648)  
AUTHORS Goodwin,R.G., Smith,C.A., Armitage,R.J. and Gruss,H.  
TITLE CD30 ligand conjugates  
JOURNAL Patent: US 5753203-A 22 19-MAY-1998;  
FEATURES Location/Qualifiers  
source 1..648  
BASE COUNT 175 a 166 c 136 g 171 t  
ORIGIN

Query Match 60.7%; Score 402.2; DB 9; Length 648;  
Best Local Similarity 79.0%; Pred. No. 3.5e-110;  
Matches 492; Conservative 0; Mismatches 128; Indels 3; Gaps 1;

QY 44 CGAGGCCCTGGAGAGCACAAGTCGAGCTACTTCTACCTCAGCACCCGCGACTGG--- 100  
DB 26 CCAGCCACTGGGACCAAGCCGAGCTATTCTATTGACCAAGCGACTCTGGCTC 85  
QY 101 TGTGCTTGTGTGGCAGTGGGATCATCTGGTACTGGTAGTCCAGAAAAGGACTCCA 160  
DB 86 TGTGCTTGTGTTCACGGTGGCCACTATTATGTTGGTTCAGAGGCGGACTCCA 145  
QY 161 CTCCAAATFACAACTGAGAGGCCGCCCTTAAAGAGGAGAAATGCTCAGAGGATCTCTTCT 220  
DB 146 TTCCCACTACCTGACAACTGCTCCCTCAAGAGGAGAAATGCTCAGAGGACTCTTAT 205  
QY 221 GTACCCCTGAAAGTACTCCATCCAAAGAGTCAATGGGCTTACCTCCAAAGTGTCAAAGCATC 280  
DB 206 GTATCTCTGAAAGAGCTCCATTCAGAAAGTCAATGGGCTTACCTCCAAAGTGTCAAAGCATC 265  
QY 281 TCACAAATACCAAACTGTGTAAGAGAGATGGGACCATCCAGGACTCATATACCAGG 340  
DB 266 TAAACAAACCAAGTGTCTTGGAAACAAAGATGGCAATTCCTCATGAGTCAAGATACAGG 325  
QY 341 ACGGGAACCTGATGCTCAATTCCTGGCTGTGCTTCACTGCTTGGCAACTGCAAGTTCC 400  
DB 326 ATGGGAATCTGGTCAATTCCTGGCTGTGCTTCACTGCTTGGCAACTGCAAGTTCC 385  
QY 401 TCGTGCAGTGTCAAAATCATCTGTGACCTGACATTCGAGCTCCTCATCAATTTCCAAGA 460  
DB 386 TTGTACAAATGCCAAATAATCTGTGATCTGAACTTGGAGCTTCTCATCAACAAAGCATA 445  
QY 461 TCAAAAGCAGACGTTGTAACAGTGTGAGTCTGGAGTTCAGAGTCAAGACATCTACC 520  
DB 446 TCAAAAGCAGACGCTGGTACAGTGTGAGTCTGGAGTTCAGAGTCAAGACATCTACC 505  
QY 521 AGAATCTCTCAGTCTTGTGCTGATTAATCTACAGTCAAACTCTACCATATCAGTCAGG 580  
DB 506 AGAATCTCTCAATCTTGTGCTGATTAATCTACAGTCAAACTCTACCATATCAGTCAGG 565  
QY 581 TGGATAATTTCCAGTATGGATACAAACATTTTCCCTCTTGATTAATGTCATCCGCTCT 640  
DB 566 TGGATACATTCAGTATACATACAAAGCAGCTTTCCCTCTTGAGAAATGTTGTCCATCT 625  
QY 641 TCTTATATAGTACGACTGA 663  
DB 626 TCTTATACAGTAATTCAGACTGA 648

RESULT 9  
LOCUS I16912  
DEFINITION Sequence 22 from patent US 5480981.  
ACCESSION I16912

VERSION I16912.1 GI:1251820  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 648)  
AUTHORS Goodwin,R.G., Smith,C.A., Armitage,R.J. and Gruss,H.  
TITLE CD30 ligand  
JOURNAL Patent: US 5480981-A 22 02-JAN-1996;  
FEATURES Location/Qualifiers  
source 1..648  
BASE COUNT 175 a 166 c 136 g 171 t  
ORIGIN

Query Match 60.7%; Score 402.2; DB 10; Length 648;  
Best Local Similarity 79.0%; Pred. No. 3.5e-110;  
Matches 492; Conservative 0; Mismatches 128; Indels 3; Gaps 1;

QY 44 CGAGGCCCTGGAGAGCACAAGTCGAGCTACTTCTACCTCAGCACCCGCGACTGG--- 100  
DB 26 CCAGCCACTGGGACCAAGCCGAGCTATTCTATTGACCAAGCGACTCTGGCTC 85  
QY 101 TGTGCTTGTGTGGCAGTGGGATCATCTGGTACTGGTAGTCCAGAAAAGGACTCCA 160  
DB 86 TGTGCTTGTGTTCACGGTGGCCACTATTATGTTGGTTCAGAGGCGGACTCCA 145  
QY 161 CTCCAAATFACAACTGAGAGGCCGCCCTTAAAGAGGAGAAATGCTCAGAGGATCTCTTCT 220  
DB 146 TTCCCACTACCTGACAACTGCTCCCTCAAGAGGAGAAATGCTCAGAGGACTCTTAT 205  
QY 221 GTACCCCTGAAAGTACTCCATCCAAAGAGTCAATGGGCTTACCTCCAAAGTGTCAAAGCATC 280  
DB 206 GTATCTCTGAAAGAGCTCCATTCAGAAAGTCAATGGGCTTACCTCCAAAGTGTCAAAGCATC 265  
QY 281 TCACAAATACCAAACTGTGTAAGAGAGATGGGACCATCCAGGACTCATATACCAGG 340  
DB 266 TAAACAAACCAAGTGTCTTGGAAACAAAGATGGCAATTCCTCATGAGTCAAGATACAGG 325  
QY 341 ACGGGAACCTGATGCTCAATTCCTGGCTGTGCTTCACTGCTTGGCAACTGCAAGTTCC 400  
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QY 401 TCGTGCAGTGTCAAAATCATCTGTGACCTGACATTCGAGCTCCTCATCAATTTCCAAGA 460  
DB 386 TTGTACAAATGCCAAATAATCTGTGATCTGAACTTGGAGCTTCTCATCAACAAAGCATA 445  
QY 461 TCAAAAGCAGACGTTGTAACAGTGTGAGTCTGGAGTTCAGAGTCAAGACATCTACC 520  
DB 446 TCAAAAGCAGACGCTGGTACAGTGTGAGTCTGGAGTTCAGAGTCAAGACATCTACC 505  
QY 521 AGAATCTCTCAGTCTTGTGCTGATTAATCTACAGTCAAACTCTACCATATCAGTCAGG 580  
DB 506 AGAATCTCTCAATCTTGTGCTGATTAATCTACAGTCAAACTCTACCATATCAGTCAGG 565  
QY 581 TGGATAATTTCCAGTATGGATACAAACATTTTCCCTCTTGATTAATGTCATCCGCTCT 640  
DB 566 TGGATACATTCAGTATACATACAAAGCAGCTTTCCCTCTTGAGAAATGTTGTCCATCT 625  
QY 641 TCTTATATAGTACGACTGA 663  
DB 626 TCTTATACAGTAATTCAGACTGA 648

RESULT 10  
LOCUS I69505  
DEFINITION Sequence 22 from patent US 5677430.  
ACCESSION I69505  
VERSION I69505.1 GI:2831627  
KEYWORDS Unknown.  
SOURCE

ORGANISM Unknown.  
Unclassified.  
REFERENCE 1 (bases 1 to 648)  
AUTHORS Goodwin,R.G., Smith,C.A., Armitage,R.J. and Gruss,H.  
TITLE Antibodies directed against CD30 ligand  
JOURNAL Patent: US 5677430-A 22 14-OCT-1997;  
FEATURES Location/Qualifiers  
source 1..648  
BASE COUNT 175 a 166 c 136 g 171 t  
ORIGIN

Query Match 60.7%; Score 402.2; DB 10; Length 648;  
Best Local Similarity 79.0%; Pred. No. 3.5e-110;  
Matches 492; Conservative 0; Mismatches 128; Indels 3; Gaps 1;

QY 44 CGAGGCCCTGGAGAGCACAAGTCGACGACTCTTACCTCAGCACCACCGCACTGG--- 100  
Db 26 CCAGCCACTGGGACACAGAGCCGAGCTATTTCTATTGGACCAGCCACTCTGGCTC 85  
QY 101 TGTGCTTTGTTGTGCGAGTGGCGATCATTTCTGGTACTGTGTAGTCCAGAAAAGGACTCCA 160  
Db 86 TGTGCTTTGTTGTGCGAGTGGCGATCATTTCTGGTACTGTGTAGTCCAGAAAAGGACTCCA 145  
QY 161 CTCCAATACAACTGAGAGGCCGCCCTTAAAGGAGGAAATGCTCAGAGGATCTCTTCT 220  
Db 146 TTCCCAACTCACTGACAACTGCGCCCTCAAAGGAGGAAATGCTCAGAGGATCTCTTAT 205  
QY 221 GTACCTGAAAAGTACTCCATCCAAAGAGTCAATGGCCCTACCTCCCAAGTGTCAAGCATC 280  
Db 206 GTATCCTGAAAAGTACTCCATCCAAAGAGTCAATGGCCCTACCTCCCAAGTGTCAAGCATC 265  
QY 281 TCACAATACCAAACTGTCATGGAACGAGATGGCACTCCACGAGCTCATATACAGG 340  
Db 266 TAAACAAAACCAAGTTGCTTGGACAAAGATGGCATCTCCATGGAGTCAGATATCAGG 325  
QY 341 ACGGGAACCTGATAGTCCAAATCCCTGGCTTGTACTTTCATCGTTTGGCAACTCAGTTCC 400  
Db 326 ATGGGAATCTGGTATCCAAATCCCTGGCTTGTACTTTCATCGTTTGGCAACTCAGTTTC 385  
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QY 641 TCTTATATAGTAGTCAGACTGA 663  
Db 626 TCTTATACAGTAATTCAGACTGA 648

RESULT 11  
LOCUS AR007969 705 bp DNA PAT 04-DEC-1998  
DEFINITION Sequence 7 from patent US 5753203.  
ACCESSION AR007969  
VERSION AR007969.1 GI:3967078  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 705)  
Unclassified.  
AUTHORS Goodwin,R.G., Smith,C.A., Armitage,R.J. and Gruss,H.  
TITLE CD30 ligand  
JOURNAL Patent: US 5480981-A 7 02-JAN-1996;

AUTHORS Goodwin,R.G., Smith,C.A., Armitage,R.J. and Gruss,H.  
TITLE CD30 ligand conjugates  
JOURNAL Patent: US 5753203-A 7 19-MAY-1998;  
FEATURES Location/Qualifiers  
source 1..705  
BASE COUNT 190 a 186 c 152 g 177 t  
ORIGIN

Query Match 60.7%; Score 402.2; DB 9; Length 705;  
Best Local Similarity 79.0%; Pred. No. 3.5e-110;  
Matches 492; Conservative 0; Mismatches 128; Indels 3; Gaps 1;

QY 44 CGAGGCCCTGGAGAGCACAAGTCGACGACTCTTCTTACTCAGCACCACCGCACTGG--- 100  
Db 83 CCAGCCACTGGGACACAGAGCCGAGCTATTTCTATTGGACCAGCCACTCTGGCTC 142  
QY 101 TGTGCTTTGTTGTGCGAGTGGCGATCATTTCTGGTACTGTGTAGTCCAGAAAAGGACTCCA 160  
Db 143 TGTGCTTTGTTGTGCGAGTGGCGATCATTTCTGGTACTGTGTAGTCCAGAAAAGGACTCCA 202  
QY 161 CTCCAAATACAACTGAGAGGCCGCCCTTAAAGGAGGAAATGCTCAGAGGATCTCTTCT 220  
Db 203 TTCCCAACTCACTGACAACTGTCGCCCTCAAAGGAGGAAATGCTCAGAGGATCTCTTAT 262  
QY 221 GTACCTGAAAAGTACTCCATCCAAAGAGTCAATGGCCCTACCTCCCAAGTGTCAAGCATC 280  
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QY 281 TCACAATACCAAACTGTCATGGAACGAGATGGCACTCCACGAGCTCATATACAGG 340  
Db 323 TAAACAAAACCAAGTTGCTTGGAAACAAAGATGGCATTTCCATGGAGTCAGATATCAGG 382  
QY 341 ACGGGAACCTGATAGTCCAAATCCCTGGCTTGTACTTTCATCGTTTGGCAACTCAGTTCC 400  
Db 383 ATGGGAATCTGGTATCCAAATCCCTGGCTTGTACTTTCATCGTTTGGCAACTCAGTTTC 442  
QY 401 TCGTGCAGTGTCAATCATCTCTGGACCTGACATTTGAGCTCCATCAATTCACAAG 460  
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QY 461 TCAAAAAGCAGACGTTGGTAACAGTGTGTGAGTCTGGAGTTCAGAGTAAGAATCATCTACC 520  
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QY 521 AGAATCTCTCAGTTTGTGTCATTAATACAGTCAACTTACAGTCACTATACATATCAGTCAGG 580  
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QY 641 TCTTATATAGTAGTCAGACTGA 663  
Db 683 TCTTATACAGTAATTCAGACTGA 705

RESULT 12  
LOCUS I116903 705 bp DNA PAT 03-APR-1996  
DEFINITION Sequence 7 from patent US 5480981.  
ACCESSION I116903  
VERSION I116903.1 GI:1251811  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 705)  
Unclassified.  
AUTHORS Goodwin,R.G., Smith,C.A., Armitage,R.J. and Gruss,H.  
TITLE CD30 ligand  
JOURNAL Patent: US 5480981-A 7 02-JAN-1996;

JOURNAL PA  
EATUES  
source

Qy	581	TGGATAATTTCCAGTAGTGTGATACAAACACTTTCCCTCTTTGATAAATGTGCTATCCGTCT	640
Db	737	TGGATACATTTCCAGTACATAGATACAGACCTTTCTCTTTGAGAATGTGTTGCCATCT	796
Qy	641	TCATTATAGTAGCTCAGACTGA	663
Db	797	TCATTATAGTAATTCAGACTGA	819
RESULT 15			
AF081364	AF081364	660 bp	SYN 02-AUG-1999
LOCUS	Synthetic construct CD30 ligand-exotoxin A fusion protein (CD30L-ETA fusion) mRNA, partial cds.		
ACCESSION	AF081364		
VERSION	AF081364.1	GI:5669594	
KEYWORDS	synthetic construct.		
SOURCE	synthetic construct		
ORGANISM	artificial sequence.		
REFERENCE	1 (bases 1 to 660)		
AUTHORS	Barth, S., Matthey, B., Diehl, V. and Engert, A.		
TITLE	Direct Submission		
JOURNAL	Submitted (30-JUL-1998) Med. Klinik I, LFI, Eb 4, R 703, Joseph-Stelzmann-Str. 9, Koeln, NRW 50931, Germany		
FEATURES	Location/Qualifiers		
source	1..660		
gene	/organism="synthetic construct"		
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CDs	1..>660		
	/gene="CD30L-ETA fusion"		
	1..>660		
	/gene="CD30L-ETA fusion"		
	/note="fusion protein of Homo sapiens CD30 ligand and Pseudomonas aeruginosa deletion mutant of exotoxin A (ETA)".		
	/codon_start=1		
	/transl_table=11		
	/product="CD30 ligand-exotoxin A fusion protein"		
	/protein_id="AADA6392.1"		
	/db_xref="GI:5669593"		
	/translation="MKYLLPTAAAGLLLLAAQAPAMGHHHHHHHHSSGHHDDDDK HMKLLQTKRAPKFKSWAYLQVAKHLNKTKLSWKNKGILHGVRQDGNLVIQPPLGYL IICQLQPLVOCPPNSVDLKELLINKHKIKQALVTVCESGMQTKRHYQNLQSPLLDLY QVNTTISVNVDTQYIDTSTFPLENLVSLFLYSNDELASGGPEGSLAALTAHQACH LP"		
BASE COUNT	176 a	180 c	143 g 161 t
ORIGIN			
Query Match	47.38;	Score 313.4;	DB 56; Length 660;
Best Local Similarity	80.99;	Pred. No. 2.le-83;	
Matches 365;	Conservative 0;	Mismatches 86;	Indels 0; Gaps 0;
Qy	210	GGATCTCTTCGTACCTCGAAAGTACTCCATCAAGAAAGTCATGGGCGCTACCTCCCAAGT	269
Db	138	GAAGCTTTATGTATCTCGTAAAGAGCACCATTCAAGAAAGTCATGGGCGCTACCTCCCAAGT	197
Qy	270	GTCAAGCATCTCAACATACCAACTGTCTATGGAAGCAAGATGGCACCATTCCACGAGCT	329
Db	198	GGCAAGCATCTAAACAAAACCAAGTTGTCTTGTGGAACAAAGATGGCATTTCTCCCATGAGT	257
Qy	330	CATATACAGACGGGAACCTGATAGTCCCAATTCCTCGGCTGTGACTTCATCGTTTGCCA	389
Db	258	CAGATATCAGGATGGGAATCTGGTGATCCCAATTCCTCGTGTGACTTCATTCATTTGCCA	317
Qy	390	ACTCAGTTCTCGTCGAGTGCTCAAAATCATCTGTGGACCTCGACATTCGAGCTTCCTCAT	449
Db	318	ACTCAGTTCTCTGTCACATGCCCAATTAATTCGTGCACTGAAGTTGGAGCTTCAT	377
Qy	450	CAATTCCAAGATCAAAAAGCAGAGCTTGGTAACAGTGTGTGAGTCTGGAGTTCAAGATAA	509
Db	378	CAACAAAGCATATAAAACAGGCGCTGGTCACAGTGTGAGTCTGGAATGCAACAGAA	437





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2001, 10:29:26 ; Search time 50.89 Seconds  
(without alignments)  
571.961 Million cell updates/sec

Title: US-09-628-126-19  
Perfect score: 1141  
Sequence: 1 MQVPGSVASFWSTRPWS.....DTNTFPLDNLVSLYSSD 220

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_16.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phase.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_unclassified.\*
- 13: sp\_vertebrate.\*
- 14: sp\_virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	794.5	69.6	234	4	O43404 homo sapien
2	89.5	7.8	225	13	Q9IB42
3	89.5	7.8	401	2	P72902 synchocyst
4	89.5	7.8	847	14	Q9WIS1 human immun
5	89	7.8	169	11	Q9WV90 marmota mon
6	88	7.7	234	6	Q28320 capra hircu
7	87	7.6	896	10	Q9M9B0 arabidopsis
8	87	7.6	2013	5	Q96216 plasmodium
9	86.5	7.6	2195	3	Q02822 saccharomyc
10	86	7.5	280	6	Q9MYL6 macaca neme
11	86	7.5	674	3	Q06629 saccharomyc
12	85	7.4	699	14	Q9DP26 human immun
13	84.5	7.4	207	2	O68241 pantoea cit
14	84.5	7.4	217	11	Q9ERG6 peromyscus
15	84.5	7.4	884	10	O81069 arabidopsis
16	84	7.4	1110	10	Q9SDA5 arabidopsis
17	82	7.2	282	14	Q9IC83 kaposi's sa
18	81.5	7.1	151	5	Q9GP20 globodera r
19	81.5	7.1	304	5	Q94382 caenorhabdi

20	81.5	7.1	304	5	Q94383	Q94383 caenorhabdi
21	81	7.1	866	10	Q9SUN4	Q9SUN4 arabidopsis
22	81	7.1	1391	14	Q9DPR7	Q9DPR7 meleagrid h
23	81	7.1	1409	14	Q9ELH3	Q9ELH3 meleagrid h
24	80.5	7.1	344	10	O81781	O81781 arabidopsis
25	80	7.0	165	1	Q58685	Q58685 methanococc
26	80	7.0	232	4	Q9UIV3	Q9UIV3 homo sapien
27	80	7.0	358	14	Q71050	Q71050 human immun
28	80	7.0	369	2	Q59532	Q59532 synchocyst
29	80	7.0	400	14	O11578	O11578 human immun
30	80	7.0	403	14	O11580	O11580 human immun
31	79.5	7.0	399	14	O11584	O11584 human immun
32	79.5	7.0	889	10	Q9SNA3	Q9SNA3 arabidopsis
33	79	6.9	350	4	Q9NSP7	Q9NSP7 homo sapien
34	79	6.9	364	4	Q9HBI1	Q9HBI1 homo sapien
35	79	6.9	366	2	Q9REN2	Q9REN2 buchnera ap
36	79	6.9	402	14	O11576	O11576 human immun
37	79	6.9	412	14	O11565	O11565 human immun
38	79	6.9	902	14	Q9DHL2	Q9DHL2 yaba-like d
39	78.5	6.9	234	6	Q9TJ3	Q9TJ3 equus cabal
40	78.5	6.9	1150	3	Q02511	Q02511 saccharomyc
41	78.5	6.9	1477	3	Q74218	Q74218 candida alb
42	78	6.8	427	3	Q94386	Q94386 schizosacch
43	78	6.8	616	5	O16770	O16770 caenorhabdi
44	77.5	6.8	539	14	P88843	P88843 avian infec
45	77.5	6.8	912	10	Q9FN96	Q9FN96 arabidopsis

ALIGNMENTS

RESULT 1  
O43404 ID O43404 PRELIMINARY; PRT; 234 AA.  
AC O43404;  
DT 01-JUN-1998 (TREMREL. 06, Created)  
DT 01-JUN-1998 (TREMREL. 06, Last sequence update)  
DT 01-MAR-2001 (TREMREL. 16, Last annotation update)  
DE CD30L PROTEIN.  
GN CD30L.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98007874; PubMed=9349718;  
RA Croager E.J., Abraham L.J.;  
RT "Characterisation of the human CD30 ligand gene structure.";  
RL Biochim. Biophys. Acta 1353:231-235(1997).  
DR EMBL; AF006384; AAB97877.1; -.  
DR EMBL; AF006381; AAB97877.1; JOINED.  
DR EMBL; AF006382; AAB97877.1; JOINED.  
DR EMBL; AF006383; AAB97877.1; JOINED.  
DR InterPro; IPR000478; -.  
DR InterPro; IPR003638; -.  
DR Pfam; PF00229; TNF; 1.  
DR ProDom; PD023087; -.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
DR SMART; SM00207; TNF; 1.  
SQ SEQUENCE 234 AA; 25963 MW; 37BA5733C7911751 CRC64;

Query Match 69.6%; Score 794.5; DB 4; Length 234;  
Best Local Similarity 69.2%; Pred. No. 8.1e-69;  
Matches 153; Conservative 26; Mismatches 35; Indels 7; Gaps 2;

QY 1 MQVPGSVASFWSTRPWSRVSFYLSLTAL-VCLVAVAILLVVQKRDSPNTE 59  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 20 MHVPAGSVAS-----HLGTTSRVSFYLTATLALCLVFTVATIMLVVQRTDSIPNSPD 73  
QY 60 KAPLKGNCSEDLFTCTLKSTPSSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIV 119

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Db 74 NVPLKGGNCSEDLILKRAPEKSKWAYLQVAKHLNKTLSWNKDGILHGVRQDGNLVI 133
Qy 120 QPGLYFYICQLQFLVQCSNHSVDLTQLLINSKIKKQTLVTVCEGVSQSKNIYQNLQSOF 179
Db 134 QPGLYFYICQLQFLVQCPNNSVDLKLXELLINKHKQKLVTVCEGSMQTKHYQNLQSOF 193
Qy 180 LLHYLQVNSTISVRVDNFQYVDNTFPDLNVLVSFLYSSD 220
Db 194 LLDYLVQVNTISVVDVDTQYIDTSTFPLENVLISFLXNSD 234

RESULT 2
Q9IB42 PRELIMINARY; PRT; 225 AA.
AC Q9IB42;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE TUMOR NECROSIS FACTOR.
OS Paralicthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidae; Bothidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RA Hirono I., Nam B., Kurobe T., Aoki T.;
RT "Molecular cloning, characterization and expression of tumor necrosis
RT factor (TNF) cDNA and gene from Japanese flounder Paralicthys
RT olivaceus.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB040448; BAA94969.1; -
DR InterPro: IPR000478; -
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PR01234; TNCRSISFCT.
DR PROSITE: PS50049; TNF.2; 1.
SQ SEQUENCE 225 AA; 24965 MW; 8F947FB25FC82658 CRC64;

Query Match 7.8%; Score 89.5; DB 13; Length 225;
Best Local Similarity 25.4%; Pred. No. 0.58;
Matches 31; Conservative 23; Mismatches 57; Indels 11; Gaps 5;

Qy 33 LVCLVWVAIILVLVQKDSPTNPTTEKAPLKGNCSE--DLFCLIKSTPSK-KSWAYL- 88
Db 10 IVALCLGVLAFSWYTNKSMNTQSGTAAALSKDKCAEKTEPHNTLRQISSRAKAIHLE 69
Qy 89 ---QVSKHLNNTKLSW-NEDG---TIHGLYQDGNLIVQFGLYFIVCOLOFLVQCSNHS 141
Db 70 GRDEDETSKLNKLVKNDGLAFTQGGFELVDNHIIPRSLGYFYVQASFRVSCSDD 129
Qy 142 VD 143
Db 130 AD 131

RESULT 3
P72902 PRELIMINARY; PRT; 401 AA.
AC P72902;
DT 01-FEB-1997 (Tremblrel. 02, Created)
DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)
DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
DE HYPOTHETICAL 46.0 KDA PROTEIN.
GN SLR1066.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97061201; PubMed=8905231;
RX
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RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Suglura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synecocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
DR EMBL: D90901; BAA16918.1; -
DR InterPro: IPR001296; -
DR Pfam: PF00534; Glycos_transf_1; 1.
DR KW Hypothetical protein.
SQ SEQUENCE 401 AA; 45951 MW; 9A8C3E0C64933271 CRC64;

Query Match 7.8%; Score 89.5; DB 2; Length 401;
Best Local Similarity 26.6%; Pred. No. 1.1;
Matches 42; Conservative 13; Mismatches 50; Indels 53; Gaps 6;

Qy 71 DLFCTLKSTPSKSWAYL-----QVSKHLN-----NTKLSWNEDGTIH 108
Db 47 DAPPEIKSLPKLLWLRLPMPSPSQRAKEVIQKHANFFDIIDAOQGNLPSEK- 101
Qy 109 GLIYQDGNLIVQFGLYFIVCOLOFLVQ-----CSNHSVDLTQLLINSKIKKQTLVTV 162
Db 102 --LKFNCTLVRSVGLYAFHQFOELQVKTWNLSGNVFKLLKRLKRIKQKQN---- 155
Qy 163 CEGSVQSKNIYQNLQSOFLLHYLQVNSTISVRVDNFQIV 200
Db 156 -----QN---YLLSFQKADGIILNSDELAVY 179

RESULT 4
Q9WIS1 PRELIMINARY; PRT; 847 AA.
AC Q9WIS1;
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE ENVELOPE GLYCOPROTEIN PRECURSOR, GPI60.
OS Human immunodeficiency virus type 1.
OX Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11676;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=97NOGIL3;
RA Jonassen T.O.;
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=97NOGIL3;
RX MEDLINE=20092438; PubMed=10628816;
RA Jonassen T.O., Grinde B., Asjo B., Hasle G., Hungnes O.;
RT "Inter-subtype recombinant HIV-1 involving HIV-MAL-like and subtype H-
RT like sequence in four Norwegian cases.";
RL AIDS Res. Hum. Retroviruses 16:49-58(2000).
DR EMBL: AJ237565; CAB39923.2; -
DR InterPro: IPR000328; -
DR Pfam: PF00516; GP120; 1.
DR Pfam: PF00517; GP41; 1.
SQ SEQUENCE 847 AA; 95496 MW; E8770E4691304EB6 CRC64;

Query Match 7.8%; Score 89.5; DB 14; Length 847;
Best Local Similarity 20.9%; Pred. No. 2.4;
Matches 37; Conservative 37; Mismatches 56; Indels 47; Gaps 8;

Qy 52 DSTPNTTEKAPLKGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLI 111
Db 138 DTTNNTSIQSPQSANCSFNVTAIIRDQKQKHALFYRV----DLVSIDNNDNNTQRLI 193
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QY 112 YDQGNLIYQ-----FGLYFIV-----COQLFYQCSNHSVD- 143
Db 194 NCNFSVITQACPKVTEPIPIHYCAPAGAILKCNKNTFSGTGPCKNVSTVQCT-HGKIP 252
QY 144 -LTQLLLINSIKKQTLVTVCSGVQSKNIYQNLSQFLHY----LQVNSTISVRVDN 196
Db 253 VVSTQLLLINGSIAERVI-----IRSKNITDNTKNIIVHFNESVOINCT---RIAN 299

RESULT 5
Q9WV90 PRELIMINARY; PRT; 169 AA.
AC Q9WV90;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DE FAS LIGAND (FRAGMENT).
OS Marmota monax (Woodchuck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sclurinae;
OC Marmota.
OX NCBI_TaxID=9995;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEALTHY LIVER;
RA Hodgson P.D., Grant M.D., Michalak T.I.;
RT "Perforin and Fas/Fas ligand-mediated cytotoxicity in acute and
RL chronic woodchuck viral hepatitis.";
DR EMBL: AF152368; AAD38387.1; -.
DR InterPro: IPR000478; -.
DR Pfam: PF00229; TNF; 1.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS00049; TNF_2; 1.
DR SMART: SM00207; TNF; 1.
FT NON_TER 1
FT NON_TER 169
SQ SEQUENCE 169 AA; 19274 MW; FDB395B014717B6B CRC64;

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Query Match 7.8%; Score 89; DB 11; Length 169;
Best Local Similarity 24.1%; Pred. No. 0.48; Mismatches 42; Indels 38; Gaps 7;
Matches 33; Conservative 24;

QY 78 STPSKKS----WAYLQVSKHLNNTKLSWNE---GTIHGLIYQDGNLIYQFGLYFIVQ 130
Db 32 SSPSDKKALRAAHLTKPNSRSPLEWEDTYGISLSGVKYQKGLVINDTGLYFVYSK 91
QY 131 LQFLVQ-CSN----HSVDLTQLLINSK-----IKKQTLVTVCSG----- 166
Db 92 IYFRQSCNNQPLSHKV-----YVKNRYKYPQDLVLMCKRMNMYCTTGQMWARSYLGAVF 146
QY 167 --VQSKNIYQNLSQFL 181
Db 147 NFTSNDHLIVNSEL 163

RESULT 6
Q28320 PRELIMINARY; PRT; 234 AA.
AC Q28320;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE TNF-ALPHA.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA Takakura H., Mori Y., Tatsumi M.;

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RT "Molecular cloning of caprine TNF-alpha cDNA and its expression in
RT E.coli and insect cells.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: D86587; BAA13130.1; -.
DR HSSP: P01375; 4TSV.
DR InterPro: IPR000478; -.
DR InterPro: IPR003636; -.
DR Pfam: PF00229; TNF; 1.
DR PRINTS: PR01234; TNECROSISFCT.
DR PRODOM: PD002012; -.
DR PROSITE: PS00251; TNF_1; 1.
DR PROSITE: PS00049; TNF_2; 1.
DR SMART: SM00207; TNF; 1.
SQ SEQUENCE 234 AA; 25519 MW; 976BE33BBABB041 CRC64;

Query Match 7.7%; Score 88; DB 6; Length 234;
Best Local Similarity 24.1%; Pred. No. 0.84;
Matches 48; Conservative 38; Mismatches 89; Indels 24; Gaps 8;

QY 22 SRSFYLTSTALVCLVAVAIILVLYVYVKKDSTPTTTEKAPLKGNGCSEDLFTLKST-- 79
Db 27 SRSWCWCLSLFSF--LLVAGATTLLFCLLHFGVIGPQREEQSP-AGPSENRPLVQTLRSSQ 83
QY 80 -PSKKSHWAYLOVSKHLNNTKLSWNEGT-----IHGLIYQDGNLIYQFGLYFIVQ 134
Db 84 ASSNKPVAVHY-VANISAPGQLRWGDSYANALKANGVELKQNLVPTDGLYLYISQVLF 142
QY 135 VQ-CSNHSVDLTQLLINSIKKQTLVTVCS-----GVQSKNIYQNLSQFL 182
Db 143 GHGCPSTPLFLT-HTISRIAVSYQTKVNIILSAIKSPCHRETPEGAEPKPYEPIYQGVF 201
QY 183 YLQVNSTISVRVDNFOYVD 201
Db 202 QLEKGDRLSAEQNPYLD 220

RESULT 7
Q9M9B0 PRELIMINARY; PRT; 896 AA.
AC Q9M9B0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE F27J15.13.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA Kim C., Altafi H., Bel Q., Chin C., Chiou J., Choi E., Conn L.,
RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsy N., Nguyen M.,
RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
RA Ecker J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F27J15 from chromosome
RT I.";
RC Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RL -! SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AC016041; AAF69701.1; -.
DR InterPro: IPR000719; -.
DR InterPro: IPR001245; -.
DR InterPro: IPR001611; -.
DR InterPro: IPR002290; -.
DR Pfam: PF00069; pkinase; 1.
DR Pfam: PF00560; LRR; 3.
DR PRINTS: PR00019; LEURICHRPT.
DR PRINTS: PR00109; TYRKINASE.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.

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01-NOV-1996 (TrEMBLrel: 01, Created)  
01-NOV-1996 (TrEMBLrel: 01, Last sequence update)  
01-MAR-2001 (TrEMBLrel: 16, Last annotation update)  
VESICLE COAT PROTEIN SEC16P.  
SEC16.  
Saccharomyces cerevisiae (Baker's yeast).  
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
NCBI\_TaxID=4932;  
[1]  
SEQUENCE FROM N.A.  
MEDLINE=87089718; PubMed=3025612;  
Baker H.V.;  
"Glycolytic gene expression in Saccharomyces cerevisiae: nucleotide  
sequence of GCRI, null mutants, and evidence for expression.";  
Mol. Cell. Biol. 6:3774-3784(1986).  
[2]  
SEQUENCE FROM N.A.  
MEDLINE=88111651; PubMed=2892678;  
Velours J., Durrens P., Aigle M., Guerin B.;  
"ATP4, the structural gene for yeast F0F1 ATPase subunit 4.";  
Eur. J. Biochem. 170:637-642(1988).  
[3]  
SEQUENCE FROM N.A.  
MEDLINE=92195335; PubMed=1312673;  
Davis J.L., Kunisawa R., Thorner J.;  
"A presumptive helicase (MOR1 gene product) affects gene expression  
and is required for viability in the yeast Saccharomyces cerevisiae.";  
Mol. Cell. Biol. 12:1879-1892(1992).  
[4]  
SEQUENCE FROM N.A.  
MEDLINE=95274317; PubMed=7754704;  
Schnall R., Mannhaupt G., Stucka R., Tauer R., Ehnlé S.,  
Schwarzlose C., Vetter I., Feldmann H.;  
"Identification of a set of yeast genes coding for a novel family of  
putative ATPases with high similarity to constituents of the 26S  
protease complex.";  
Yeast 10:1141-1155(1994).  
[5]  
SEQUENCE FROM N.A.  
MEDLINE=95286583; PubMed=7768896;  
Leidich S.D., Kostova Z., Latek R.R., Costello L.C., Drapp D.A.,  
Gray W., Fassler J.S., Orlean P.;  
"Temperature-sensitive yeast GPI anchoring mutants gp12 and gp13 are  
defective in the synthesis of N-acetylglucosaminyl  
phosphatidylinositol. Cloning of the GP12 gene.";  
J. Biol. Chem. 270:13029-13035(1995).  
[6]  
SEQUENCE FROM N.A.  
MEDLINE=96017704; PubMed=7593161;  
Espenshade P., Gimeno R.E., Holzmacher E., Teung P., Kaiser C.A.;  
"Yeast SEC16 gene encodes a multidomain vesicle coat protein that  
interacts with Sec23p.";  
J. Cell Biol. 131:311-324(1995).  
[7]  
SEQUENCE FROM N.A.  
MEDLINE=97313271; PubMed=9169875;  
Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansorge W.,  
Araujo R., Aparicio A., Barrell B., Badcock K., Benes V., Botstein D.,  
Bowman S., Bruckner M., Carpenter J., Cherry J.M., Chung E.,  
Churche C., Coster F., Davis K., Davis R.W., Dietrich F.S.,  
Deliuss H., DiPaolo T., Dubois E., Dusterhoft A., Duncan M., Floeth M.,  
Fortin N., Friesen J.D., Fritz C., Goffeau A., Hall J., Hebling U.,  
Heumann K., Hilbert H., Hillier L., Hunnicke-Smith S., Hyman R.,  
Johnston M., Kalman S., Kleine K., Komp C., Kurdi O., Lashkari D.,  
Leh W.H., Lin A., Lin D., Louis E.J., Marathe R., Messenguy F.,  
Mewes H.W., Mirtipati S., Moestl D., Muller-Auer S., Namath A.,  
Nentwich U., Oefner P., Pearson D., Petel F.X., Pohl T.M.,  
Purnelle D., Schafer M., Scharfe M., Scherens B., Schramm S.,  
Schroeder M., Sdicu A.M., Tettelin H., Urrestazu L.A., Ushinsky S.,  
Vierendeels F., Vissers S., Voss H., Walsh S.V., Wambutt R., Wang Y.,  
Wedler E., Wedler H., Winnett E., Zhong W.W., Zollner A., Vo D.H.,  
Hani J.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";  
 RN Nature 387:0-0(0).  
 [8]  
 RC SEQUENCE FROM N.A.  
 RA Hall J., Ahmed A., Bussey H., Fortin N., Friesen J.D., Storms R.K.,  
 Vo D.H., Wang Y., Winnett E.;  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 [9]  
 RN SEQUENCE FROM N.A.  
 RA Bussey H.;  
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.  
 [10]  
 RN SEQUENCE FROM N.A.  
 RA Jia Y., Cherry J.M.;  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U41849; AAB68254.1; -;  
 DR SGD; S0006006; SEC16.  
 SQ SEQUENCE 2195 AA; 241694 MW; 757B7A7231BEE6F0 CRC64;

Query Match 7.6%; Score 86.5; DB 3; Length 2195;  
 Best Local Similarity 20.9%; Pred. No. 13;  
 Matches 53; Conservative 39; Mismatches 87; Indels 75; Gaps 13;  
 QY 7 SVASPRSTRP-----WRSTSRSYF-----YLSSTALVCLVVA 39  
 DB 970 SVAPRQENNPIDKIDNEALLRRQPIFHWSAANKVYAVPIPDQOYMISSIVQIKV 1029  
 QY 40 VAILLVVQKDD---STNTTEKAPLKGNCSEDLFTLKSTPSKKS-----WAYLVQ 90  
 DB 1030 TPI--DQIIKPNMLKSPGPGLSAKLKKDLTKWETIKSISENESSDMDTQWLEEM 1087  
 QY 91 SKHLNNTKLSWNEGPIHGLIYODGNLV-----OFFGLY--FIVCOLQFL--VQ 136  
 DB 1088 KL---NDKVNWK---NISLLYNSDELLMYLSOPFPNGDMIPNAYRLDINCOMRVLAFLQ 1141  
 QY 137 CSNHSV-----DLTQLLINSIKKQTLVTV-----ESGVQSKNIYONLSQFLH 182  
 DB 1142 TGNHDEALRLAKRDYAIALLVGLMGKDRWSEVTKYLYEGFTAGPNDOKELAHFLL 1201  
 QY 183 YLQV---NSTISVR 193  
 DB 1202 IFQVFGNSKMAIK 1215

RESULT 10  
 Q9MYL6 PRELIMINARY; PRT; 280 AA.  
 AC Q9MYL6;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE FAS LIGAND  
 GN PT-FASL OR CM-FASL OR RM-FASL.  
 OS Macaca nemestrina (Pig-tailed macaque),  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Macaca.  
 OC NCBI\_TaxID=9545, 9541, 9544;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC SPECIES-M. nemestrina; STRAIN-PIG-TAILED MONKEY;  
 RA Kirii Y., Inoue T., Yoshino K.;  
 RT "Pig-tailed monkey Fas ligand mRNA, complete cds.";  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RN SEQUENCE FROM N.A.  
 RC SPECIES-M. fascicularis; STRAIN-CYNOMOLGUS MONKEY;  
 RA Kirii Y., Inoue T., Yoshino K.;  
 RT "Cynomolgus monkey Fas ligand mRNA, complete cds.";  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.

[3]  
 RN SEQUENCE FROM N.A.  
 RC SPECIES=M. mulatta; STRAIN-RHESUS MONKEY;  
 RA Kirii Y., Inoue T., Yoshino K.;  
 RT "Rhesus monkey Fas ligand mRNA, complete cds.";  
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB035140; BAA90296.1; -;  
 DR EMBL; AB035138; BAA90294.1; -;  
 DR EMBL; AB035139; BAA90295.1; -;  
 DR InterPro; IPR000478; -;  
 DR Pfam; PF00229; TNF\_1;  
 DR PRINTS; PR01234; TNFCROSISFCT.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 SQ SEQUENCE 280 AA; 31367 MW; F0B284D61A132EB4 CRC64;

Query Match 7.5%; Score 86; DB 6; Length 280;  
 Best Local Similarity 21.3%; Pred. No. 1.6;  
 Matches 44; Conservative 35; Mismatches 64; Indels 64; Gaps 10;  
 QY 34 VCLVAVAIILVWV-----QKQDSTPNTTEKAPLKGNCSEDLFTLKLS--- 78  
 DB 80 LCLLVFMFVLVALVGLGLGMFQLFLQK-----ELAELESTSQKHTASSLEKQIG 131  
 QY 79 ----TPSKKSW---AYLQVSKHLNNTKLSWNEGDI---HGLIYODGNLVQFGLYFIV 128  
 DB 132 HPSPPPEKKEQKVAHLTGKPNRSMPLEWEDTGYIVLLSGVYKKGGLVINETGLYEVY 191  
 QY 129 COLQFLQV-CSN---HSDVLTQLLINSK-----IKKQTLVTVCSG----- 166  
 DB 192 SKVFRGQSCNPLSHKV-----YMRNSKYPQDLVMEKGMMSYCTTGQWHAHSSYLGA 246  
 QY 167 ----VQSKNIYONLSQFLHYLVQVNST 189  
 DB 247 VFNLTSADHLVNVSELSLVNFESQT 273

RESULT 11  
 Q06629 PRELIMINARY; PRT; 674 AA.  
 AC Q06629;  
 DT 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
 DE SIMILARITY TO STREPTOCOCCUS PROTEIN V.  
 GN D9740.10 OR PLO2.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OC NCBI\_TaxID=4932;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,  
 Favell A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,  
 Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,  
 Johnston L., Langston Y., Latreille P., Le T., Mardis E., Meneses S.,  
 Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,  
 Taich A., Trevaskis E., Vignati D., Wilcox L., Wohlman P., Vaudin M.,  
 Wilson R., Waterston R.;  
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RN SEQUENCE FROM N.A.  
 RA Ding H.;  
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RN SEQUENCE FROM N.A.  
 RA Waterston R.;  
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
 [4]  
 RN SEQUENCE FROM N.A.  
 RA Jia Y., Cherry J.M.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.

RESULT 13  
O68241  
IID O68241  
AC O68241; PRELIMINARY; PRT; 208 AA.

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Query Match      7.4%  Score 84.5; DB 11; Length 217;
Best Local Similarity 23.6%  Pred. No. 1.7;
Matches 52; Conservative 37; Mismatches 92; Indels 39; Gaps 11;

QY  5  PGSVASPRWSTRPWRSTRSYFVLS--TTALVCLVAVAIILVLVQKKDSTPTNTEKAPL 63
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   10  PKRAWCPONSRCIGCLSLPSFLVAGAGTTFLCLL-----NEGVTCPDPEKFPN--NIP 62
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |

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Search completed: September 5, 2001, 10:29:28  
Job time: 403 sec

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QY 64 KGCNCSEDLFCTLKST---PSKSWAYLQVSKHLNNTKLSWNEDGT-----IHGLIYODGN 116
Db 63 IGSMAQT---LTLRSSQSSDKPVAHV-VANHOVDQLEWLSRRANALLANGMDLKDNQ 118
QY 117 LIVQPGPLYFVCQQLFVQ-CSSN-----HSVD-----LTLQLLINSKIKKQTLVT 161
Db 119 LIVPADGLVLYVQVLFKQGCSCNYLLTHTVSRFAVSIEDKVNLLSAIKSPCKET--- 175
QY 162 VCESGVQSKNIYONLSQFLHLHYLOVNSTISVRVDNFQYVD 201
Db 176 --PEGSELKPWEPIYLGGVFQLEKGDRLSAEVLNPKYLD 213
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## RESULT 15

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081069
ID 081069 PRELIMINARY; PRT; 884 AA.
AC 081069;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE PUTATIVE RECEPTOR PROTEIN KINASE.
GN T914.7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
RA Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
RT "Arabidopsis thaliana chromosome II BAC T914 genomic sequence.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AC005315; AAC33227.1; -.
DR InterPro; IPR000719; -.
DR InterPro; IPR000871; -.
DR InterPro; IPR001611; -.
DR InterPro; IPR002290; -.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00560; LRR; 2.
DR PROSITE; PS00146; BETA_LACTAMASE_A; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR SMART; SM00220; S_TKc; 1.
KW ATP-binding; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 884 AA; 98755 MW; E354E899EAAE48BE CRC64;
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Query Match 7.4%; Score 84.5; DB 10; Length 884;
Best Local Similarity 25.1%; Pred. No. 7.6; Mismatches 51; Gaps 12;
Matches 52; Conservative 28; Indels 76;

QY 29 STTALVCLVAVAIILVVLVQKKDSTPNTTEKAPL-----KGCNC-SEDLFCTLKSTPSK 82
Db 512 SAASLVVVVVA--LFFVRKKKSPSNLHAPSPMPVNPNGHNSQSESF-----TSKK 564
QY 83 KSWAYLQVSKHLNNTKLSWNEDG---TIHGLIYODGNLIVQFPGLYFIVCQQLFVQCSN 139
Db 565 IRFTYSEVQEMTNFQKALGEGGFVVYHGFV---NVIEQ-----VAVKLLSQSSS 612
QY 140 H-----SVDLTLQLLINSKIKKQTLVTVCESGVQSKNIYQ-----NLSQFL-----H 182
Db 613 QGYKHFKAEVVELLMRY---HHINLVSLVGYCDEGEHALIYEYMPNGDLKQHLGSKRHGGF 669
QY 183 YLQVNSTISVRVD---NFOYVDNTFFP 206
Db 670 VLSWESRLKIVLDAALGLELYLHTGCVF 696
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2001, 10:29:51 ; Search time 19.38 Seconds  
(without alignments)  
388.865 Million cell updates/sec

Title: US-09-628-126-19

Perfect score: 1141

Sequence: 1 MQVQGSVASPWRTRPWS.....DTNFTPLDNVLSFLYSSD 220

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1141	100.0	239	1	TNF8_MOUSE
2	814.5	71.4	234	1	TNF8_HUMAN
3	109	9.6	279	1	FASL_MOUSE
4	91	8.0	278	1	FASL_RAT
5	88.5	7.8	309	1	41BL_MOUSE
6	87.5	7.7	235	1	TNFA_PERLE
7	86.5	7.6	2194	1	SC16_YEAST
8	85	7.4	291	1	TN10_MOUSE
9	84.5	7.4	233	1	TNFA_MACMU
10	84.5	7.4	525	1	C307_DROME
11	84	7.4	281	1	FASL_HUMAN
12	83.5	7.3	201	1	TNFB_VACEU
13	83.5	7.2	965	1	AMPN_MOUSE
14	82	7.2	234	1	TNFA_SHEEP
15	81.5	7.1	233	1	TNFA_CANFA
16	81.5	7.1	233	1	TNFA_MACFA
17	81	7.1	460	1	ENV_HV123
18	80.5	7.1	233	1	TNFA_FAPHU
19	80	7.0	1376	1	RPOD_ARATH
20	79	6.9	229	1	TNFA_CEREL
21	79	6.9	851	1	NUD1_YEAST
22	78.5	6.9	234	1	TNFA_HORSE
23	78.5	6.9	235	1	TNFA_RAT
24	78.5	6.9	1150	1	IRRI_YEAST
25	78	6.8	856	1	ENV_HV1MN
26	77.5	6.8	178	1	IL10_MACFA
27	77.5	6.8	463	1	YK3_YEAST
28	77.5	6.8	1583	1	MISA_SCHPO
29	77	6.7	795	1	SYFB_BUCAI
30	76.5	6.7	317	1	TN11_HUMAN
31	76.5	6.7	345	1	OPCM_BOVIN
32	76.5	6.7	507	1	C392_DROME
33	76.5	6.7	1073	1	HSER_PIG

#### ALIGNMENTS

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RESULT 1
TNF8_MOUSE
ID TNF8_MOUSE STANDARD; PRT: 239 AA.
AC P32972;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD30 LIGAND (CD30-L).
GN TNFSF8 OR CD30LG OR CD30L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=93313964; PubMed=8391931;
RA Smith C.A., Gruess H.-J., Davis T., Anderson D., Farrah T.,
RA Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA Grabstein K.H., Gliniak B., McAllister I.B., Fanslow W., Alderson M.,
RA Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.;
RA "CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
RT ligand defines an emerging family of cytokines with homology to
RT TNF".
RT Cell 73:1349-1360(1993).
CC -!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
CC T CELLS.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L09754; AAA74595.1; -
CC PIR: B40710; B40710.
CC MGI: MGI:88328; Tnfsf8.
CC InterPro: IPR000478; -.
CC Pfam: PF00229; TNF; 1.
CC PROSITE: PS00251; TNF.1; 1.
CC PROSITE: PS50049; TNF.2; 1.
CC Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
CC DOMAIN 1 43
CC TRANSMEM 44 67
CC FT DOMAIN 68 239
CC FT CARBOHYD 75 75
CC FT CARBOHYD 86 86
CC FT CARBOHYD 114 114
CC FT CARBOHYD 158 158
CC FT CARBOHYD 194 194
CC FT CARBOHYD 206 206
CC FT CARBOHYD 239 AA; 26519 MW; 29003157DD425159 CRC64;
CC SEQUENCE
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34 76 6.7 234 1 TNFA_CAVPO
35 76 6.7 520 1 C4P2_DROME
36 75.5 6.6 178 1 IL10_CERTO
37 75.5 6.6 1178 1 PH81_YEAST
38 75 6.6 179 1 I10H_HSV2
39 75 6.6 533 1 INV_DEBOC
40 75 6.6 2136 1 YCF2_MARPO
41 74.5 6.5 233 1 TNFA_HUMAN
42 74.5 6.5 284 1 YND3_YEAST
43 74.5 6.5 383 1 COS7_YEAST
44 74.5 6.5 488 1 CWF8_SCHPO
45 74.5 6.5 584 1 MUTL_BUCAI
P51435 cavia porce
Q95557 drosophila
P46651 cercoebus
P17442 saccharomyc
Q89451 equine herp
P24153 debaryomyce
P09975 marchantia
P01375 homo sapien
P39664 saccharomyc
Q07788 saccharomyc
O14011 schizosacch
P57633 buchnera ap
```

```

Query Match          100.0%; Score 1141; DB 1; Length 239;
Best Local Similarity 100.0%; Pred. No. 1.7e-96;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MOVPGSVASPMRSTRPWRSTRSYFYLSSTALVCLVAVAILLVVQKDSPTNTEK 60
   |||||||
DB 20 MOVPGSVASPMRSTRPWRSTRSYFYLSSTALVCLVAVAILLVVQKDSPTNTEK 79
   |||||||

QY 61 APLKGGNCSEDLCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTHGLIYQDGNLIV 120
   |||||||
DB 80 APLKGGNCSEDLCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTHGLIYQDGNLIV 139
   |||||||

QY 121 FPGLYFIVCOLQFLVQCSNHSVDLTQLLINSKIKKOTLVTVCSGVQSKNIYONLSQFL 180
   |||||||
DB 140 FPGLYFIVCOLQFLVQCSNHSVDLTQLLINSKIKKOTLVTVCSGVQSKNIYONLSQFL 199
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QY 181 LHYLVQNSTISVRVDFQYVDYDNTFPLDNLVSLVFLYSSD 220
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DB 200 LHYLVQNSTISVRVDFQYVDYDNTFPLDNLVSLVFLYSSD 239
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RESULT 2
TNF8_HUMAN
ID TNF8_HUMAN STANDARD; PRT; 234 AA.
AC P32971;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE CD30 LIGAND (CD30-L) (CD153 ANTIGEN).
GN TNFSF8 OR CD30LG OR CD30L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93313964; PubMed=8391931;
RA Smith C.A., Guess H.-J., Davis T., Anderson D., Farrah T.,
RA Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,
RA Grabstein K.H., Gliniak B., McAllister I.B., Fanslow W., Alderson M.,
RA Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.;
RT "CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose
RT ligand defines an emerging family of cytokines with homology to
RT TNF."
RL Cell 73:1349-1360(1993).
CC -!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF
CC T CELLS.
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD153 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd153.htm".
CC -----
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CC -----
DR EMBL; L09753; AAA74594.1; -.
DR PIR; A40710; A40710.
DR MIM; 603875; -.
DR InterPro; IPR000478; -.
DR Pfam; PF00229; TNF; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT DOMAIN 1 37 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 38 62 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 63 234 EXTRACELLULAR (POTENTIAL).

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FT CARBOHYD 81 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 109 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 201 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 234 AA; 26017 MW; C653615682305B1B CRC64;

Query Match          71.4%; Score 814.5; DB 1; Length 234;
Best Local Similarity 70.6%; Pred. No. 6.8e-67;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

QY 1 MOVPGSVASPMRSTRPWRSTRSYFYLSSTALVCLVAVAILLVVQKDSPTNTEK 59
   |||||||
DB 20 MHVPAGSVAS-----HLGTTSSRSFYLTATLALCLVFTVATIMLVVQRTDSIPNSPD 73
   |||||||

QY 60 KAPLKGGNCSEDLCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTHGLIYQDGNLIV 119
   |||||||
DB 74 NVPLKGGNCSEDLCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTHGLIYQDGNLIV 133
   |||||||

QY 120 QPGLYFIVCOLQFLVQCSNHSVDLTQLLINSKIKKOTLVTVCSGVQSKNIYONLSQF 179
   |||||||
DB 134 QPGLYFIVCOLQFLVQCPNNSVDLKLLELINKKKKQALVTVCSGQTKHYVQNLQSF 193
   |||||||

QY 180 LHYLVQNSTISVRVDFQYVDYDNTFPLDNLVSLVFLYSSD 220
   |||||||
DB 194 LLDYLVQNTTISVRVDFQYVDYDNTFPLENVLISFLYNSD 234
   |||||||

RESULT 3
FASL_MOUSE
ID FASL_MOUSE STANDARD; PRT; 279 AA.
AC P41047; O61217; Q9R1F2;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FAS ANTIGEN LIGAND.
DE TNFSF6 OR APTLIG1 OR FASL OR GLD.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=94185175; PubMed=7511063;
RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,
RA Suda T., Nagata S.;
RT "Generalized lymphoproliferative disease in mice, caused by a point
RT mutation in the Fas ligand."
RL Cell 76:969-976(1994).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.
RC STRAIN=C57BL/6;
RX MEDLINE=95388076; PubMed=7544870;
RA Peitsch M.J., Tschopp J.J.;
RT "Comparative molecular modelling of the Fas-ligand and other members
RT of the TNF family."
RL Mol. Immunol. 32:761-772(1995).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RX MEDLINE=95196085; PubMed=7889405;
RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,
RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;
RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a
RT TNF family gene cluster."
RL Immunity 1:131-136(1994).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM FASL).
RC STRAIN=BALB/C;
RA Fenner M.H., Shioda T., Isselbacher K.J.;
RT "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in
RT two amino acids."
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

```

Query Match 9.6%; Score 109; DB 1: Length 279;  
Best Local Similarity 26.2%; Pred. No. 0.0079;  
Matches 37; Conservative 28; Mismatches 46; Indels 30; Gaps 7;

QY 78 STPSKK-----SWAYLOVSKHLNNTKLSWED--GN--IHGLLYODGNLIVFPGLGYFIVCQ 130  
||||| | | | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
DB 133 STPSKKKEPRVAHLTGNPHRSRTPLEWEDTYGTALISGVKRYKGGVLINETGLYFYVK 192  
||| | | | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
QY 131 LQFIUVO-CNSHSVDLTQLLLNSK-----IKKTQVTVCESG-----VQ 168  
| | | | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
DB 193 VYFRQCSCNNQPNHNKYVMR-NSKYPEDLVLMSEKRLNYCTTGQIWAHSSYLGAVERNLS 251  
: : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
QY 169 SKNIYQNLSQFLHYLQVNST 189  
: : | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
DB 252 ADHLYVNIQSLSLNFEESKT 272

RESULT 4  
ID FASL\_RAT STANDARD; PRT; 278 AA.  
AC P36940;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE FAS ANTIGEN LIGAND.  
GS TNFSF6 OR APTILG1 OR FASL.  
ON Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_Taxid=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94084792; PubMed=7505205;  
SA Suda T., Takahashi T., Golstein P., Nagata S.;  
RT "Molecular cloning and expression of the Fas ligand, a novel member  
of the tumor necrosis factor family.";  
RL Cell 75:1169-1178(1993).  
CC -1- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT  
TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN  
CYTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.  
CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF  
PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE  
T CELLS, OR BOTH.  
CC CC  
CC -1- SUBUNIT: HOMOTRIMER (PROBABLE).  
CC CC  
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED  
INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL  
SURFACE.  
CC CC  
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND  
THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES,  
KIDNEY AND LUNG.  
CC CC  
CC -1- INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.  
CC CC  
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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or send an email to licensed@isb-sib.ch).

-----  
CC EMBL: U03470; AAC52129.1; -  
DR InterPro: IPR000478; -  
DR Pfam: PF00229; TNF\_1.  
DR PROSITE: PS00251; TNF\_1; 1.  
DR PROSITE: PS0049; TNF\_2; 1.  
KW Cytochrome; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis.  
FT DOMAIN 1 77 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 78 99 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
FT DOMAIN 100 278 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 4 69 PRO-RICH.  
FT DOMAIN 45 58 POLY-PRO.  
FT DISULFID 199 230 BY SIMILARITY.

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RESULT 5
ID 41BL_MOUSE
ID 41BL_MOUSE STANDARD; PRT; 309 AA.
AC P41274;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 4-1BB LIGAND (4-1BBL).
GN TNFSF9 OR LY63L OR CD137L OR CD157L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=T-cell;
RX MEDLINE=94009225; PubMed=8405064;
RA Goodwin R.G., Din W.S., Davis-Smith T., Anderson D.M., Gimpel S.D.,
RA Sato T.A., Maliszewski C.R., Brannan C.I., Copeland N.G.,
RA Jenkins N.A., Farrah T., Armitage R.J., Fanslow W.C., Smith C.A.;
RT "Molecular cloning of a ligand for the inducible T cell gene 4-1BB: a
RT member of an emerging family of cytokines with homology to tumor
RT necrosis factor.";
RL Eur. J. Immunol. 23:2631-2641(1993).
CC -!- FUNCTION: INDUCES THE PROLIFERATION OF ACTIVATED PERIPHERAL BLOOD
CC T CELLS. MAY HAVE A ROLE IN ACTIVATION-INDUCED CELL DEATH (AICD).
CC MAY PLAY A ROLE IN COGNATE INTERACTIONS BETWEEN T CELLS AND
CC B CELLS/MACROPHAGES.
CC -!- SUBUNIT: HOMODIMER (TYPE II).
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
-----
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EMBL: L15435; AAA39435.1; -.
MGD: MGI:1101058; tnfsf9.
InterPro: IPR000478; -.
Pfam: PF00229; TNF; 1.
PROSITE: PS00251; TNF.1; 1.
PROSITE: PS50049; TNF.2; 1.
Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
DOMAIN 1 82 CYTOPLASMIC (POTENTIAL).
TRANSMEM 83 103 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
DOMAIN 104 309 EXTRACELLULAR (POTENTIAL).
FT FT

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DR Pfam: PF00229; TNF; 1.  
 DR PRINTS: PRO1234; TNECROSISFCT.  
 DR PRINTS: PRO1235; TNFALPHA.  
 DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS0049; TNF\_2; 1.  
 KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.  
 FT PROPEP 1 79  
 FT CHAIN 80 235  
 FT TRANSMEM 36 56  
 FT DISULFID 148 179  
 FT CARBOHYD 86 86  
 SQ SEQUENCE 235 AA; 25822 MW; 235A5CF9F9AC624 CRC64;  
 BY SIMILARITY.  
 TUMOR NECROSIS FACTOR.  
 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
 BY SIMILARITY.  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 Query Match 7.7%; Score 87.5; DB 1; Length 235;  
 Best Local Similarity 23.6%; Pred. No. 0.57;  
 Matches 52; Conservative 38; Mismatches 91; Indels 39; Gaps 11;  
 QY 5 PGSVASPRWSTPRWSTSRYSYLS--TTALVCLVAVAILVVLVQKSTPTTEKAPL 63  
 DB 18 PKKAWGPQNSRCCLSLFSLVAGATTLFCLL---NFGVIGPQREKFPN---NLPI 70  
 QY 64 KGCNCSDELFTLKST---PSKSWAYLOVSKHLNNTKLSWNEDGT---IHGLIYODGN 116  
 DB 71 IGMAQT---LTLRSSQNSDKPVAVH-VANQVDEQLWLSRGANALLANGMDLKDQ 126  
 QY 117 LIVQPGLYFYICQLQFLVQ-CSN-----HSVD-----LTLQLLINSKIKKQTLVT 161  
 DB 127 LVIPADGLYLVYQVLFKGGSSVYLLTHTVSRAVSVEDKVNLLSAIKSPCKET--- 183  
 QY 162 VCESGVQSNKIYONISQFLHLHYLVNSTISVRVDFQYVD 201  
 DB 184 --PEGSELKPWEPIYGLGVQLEKGRDLRSAEYNLPKYLD 221  
 RESULT 7  
 SC16\_YEAST STANDARD; PRT; 2194 AA.  
 AC P48415;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE MULTIDOMAIN VESICLE COAT PROTEIN.  
 GN SEC16 OR YPL085W.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96017704; PubMed=7593161;  
 RA Espenshade P., Gimeno R.E., Holzmacher E., Teung P., Kaiser C.A.;  
 RT "Yeast SEC16 gene encodes a multidomain vesicle coat protein that  
 interacts with Sec23p.";  
 RL J. Cell Biol. 131:311-324(1995).  
 CC -!- FUNCTION: INVOLVED IN THE BUDDING OF TRANSPORT VESICLE FROM THE  
 ENDOPLASMIC RETICULUM. THE C-TERMINAL INTERACTS WITH SEC23 AND  
 WITH THE CYTOSOLIC DOMAIN OF SED4. COULD THEREFORE BE A  
 CC CONSTITUENT OF COPII VESICLE COAT. N-TERMINAL OVEREXPRESSION  
 CC CAUSES A LETHAL SECRETION DEFECT.  
 CC -!- SUBCELLULAR LOCATION: ON THE ENDOPLASMIC RETICULUM AND ON VESICLES  
 CC WHICH BUD FROM IT.  
 CC  
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 CC EMBL; U23819; AAC49088.1;  
 CC SGD; S0006006; SEC16.

KW Transport; Protein transport; Golgi stack; Endoplasmic reticulum.  
 FT MUTAGEN 1058 1058 L->S: IN SEC16-4; TS ACCUMULATION OF ER  
 MEMBRANES.  
 FT MUTAGEN 1083 1083 L->P: IN SEC16-3; TS ACCUMULATION OF ER  
 MEMBRANES.  
 FT MUTAGEN 1088 1088 L->P: IN SEC16-2; TS ACCUMULATION OF ER  
 MEMBRANES.  
 FT MUTAGEN 1230 1230 W->R: IN SEC16-1; TS ACCUMULATION OF ER  
 MEMBRANES.  
 SQ SEQUENCE 2194 AA; 241613 MW; BB1E02D2AD4683E3 CRC64;  
 Query Match 7.6%; Score 86.5; DB 1; Length 2194;  
 Best Local Similarity 20.9%; Pred. No. 10;  
 Matches 53; Conservative 39; Mismatches 87; Indels 75; Gaps 13;  
 QY 7 SVASPRWSTPRWSTSRYSYLS--TTALVCLVAVAILVVLVQKSTPTTEKAPL 39  
 DB 969 SVASPRWSTPRWSTSRYSYLS--TTALVCLVAVAILVVLVQKSTPTTEKAPL 1028  
 QY 40 VAILVVLVQKST---STPNTTEKAPLKGNCSEDLFTLKSTPSKKS-----WAYLQV 90  
 DB 1029 TPI--DQIIKPNMCLKSPFGLGSAKAKKDLTKWMTTKSISENESSTDMTITWOLLE 1086  
 QY 91 SKHLNNTKLSWNEDGTIHGLIYODGNLIV-----QFPGLY--FIVQLQFL--VQ 136  
 DB 1087 KL--NOKVNMK---NISKLLYNSDELLMYLSQPPNGMDIPNAYRLDINQMRYLAF 1140  
 QY 137 CSNHSV-----DLTLQLLINSKIKKQTLVTVC-----ESGVQSNKIYONISQFL 182  
 DB 1141 TGNHDEALRLALSRDYAIALLVGLMGRKDRWSEVIQKLYEGFTAGPDNDOKELAHF 1200  
 QY 183 YLQV---NSTISVR 193  
 DB 1201 IFQVFGVGNKMAIK 1214  
 RESULT 8  
 TN10\_MOUSE STANDARD; PRT; 291 AA.  
 AC P50592;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE TUMOR NECROSIS FACTOR LIGAND SUPERFAMILY MEMBER 10 (TNF-RELATED  
 DE APOPTOSIS INDUCING LIGAND) (TRAIL PROTEIN).  
 GN TNFSF10 OR TRAIL.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=9611955; PubMed=8777713;  
 RA Wiley S.R., Schooley K., Smolak P.J., Din W.S., Huang C.-P.,  
 RA Nicholl J.K., Sutherland G.R., Davis-Smith T., Rauch C., Smith C.A.,  
 RA Goodwin R.G.;  
 RT "Identification and characterization of a new member of the TNF  
 RT family that induces apoptosis.";  
 RL Immunity 3:673-682(1995).  
 CC -!- FUNCTION: INDUCES APOPTOSIS.  
 CC -!- SUBUNIT: HOMOTRIMER (POTENTIAL).  
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN (POTENTIAL).  
 CC -!- TISSUE SPECIFICITY: WIDESPREAD.  
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC  
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 CC EMBL; U23819; AAC49088.1;  
 CC SGD; S0006006; SEC16.

RESULT	9
TNFA_MACMU	
ID	TNFA_MACMU STANDARD; PRRT; 233 AA.
AC	P48094;
DT	01-FEB-1996 (Rel. 33, Created)
DT	01-FEB-1996 (Rel. 33, Last sequence update)
DT	15-JUL-1999 (Rel. 38, Last annotation update)
DE	TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN	TNF OR TNFA.
OS	Musca muscatta (Rhesus macaque).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Euthera; Primates; Catarrhini; Cercopithecidae;
OX	Cercopithecinae; Macaca.
OX	NCBI_TaxID=9544;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=96003435; PubMed=7561102;
RT	Villinger F.J.; Brar S.S., Wayne A.E., Chikkala N., Ansari A.A.;
RA	*Comparative sequence analysis of cytokine genes from human and nonhuman primates.*;
RL	J. Immunol. 155:3946-3954(1995).
CC	-!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHECTIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN CONDITIONS.
CC	-!- SUBUNIT: HOMOTRIMER.
CC	-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM.
CC	-!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTEOLYTIC PROCESSING.
CC	

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CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
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CC -----
CC EMBL; U19850; AAA86712.1; -.
CC DR HSP; P01375; ITNF.
CC DR InterPro; IPR000478; -.
CC DR InterPro; IPR002959; -.
CC DR Pfam; PF00229; TNF; 1.
CC DR PRINTS; PR01234; TNECROSISFCT.
CC DR PRINTS; PR01235; TNFALPHA.
CC DR PROSITE; PS00251; TNF_1; 1.
CC DR PROSITE; PS00049; TNF_2; 1.
CC KW Cytokine; Cytotoxin; transmembrane; Glycoprotein; Signal-anchor.
CC FT PROPEP 1 76 BY SIMILARITY.
CC FT CHAIN 77 233 TUMOR NECROSIS FACTOR.
CC FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
CC FT DISULFID 145 177 BY SIMILARITY.
CC FT SEQUENCE 233 AA; 25630 MW; 9F6F85050595FD59 CRC64;
CC -----
Query Match 7.4%; Score 84.5; DB 1; Length 233;
Best Local Similarity 23.5%; Pred. No. 1.1;
Matches 50; Conservative 39; Mismatches 97; Indels 27; Gaps 10;

Qy 5 PGSVASPRWTRPWRSTRSYFYLS-TTALVCLVVAIVLVLVQKKDSTPNTKAPL 63
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
18 PRKTAGQGSRRRCWFLSLFSLFVAGATTLFCLL-----HFGVIGPQREFFPKDPSLISPL 73

Qy 64 KGGNCSEDLCTLKSTPSKKSWAYLQVSKHLNNTKLKW-NEDGT--IHGLIYODGNLIV 119
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
74 AQAVRSS-----SRTPSDKPVAHV-VANPQAEQGLQWLRNANALLANGVELTDNLVV 126

Qy 120 QFPGLYFIVQLOFLVQ-CSNHSYDLT--LQLLINSKIKKQTLVTY---CE-----SCVQ 168
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
127 PSEGLYLIYSOVLPKGGCPSNHVLLHTTISRIAVSYQTKVLLLSAIKSPCQRETPEGAE 186

Qy 169 SKNIYQNLSPFLHYLQVNSTISVRVDNFOYVD 201
Db | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
187 AKPWYEPYILGGVFOLEKGRLSAEINLPDYLD 219

RESULT 10
C307_DROME STANDARD; PR; 525 AA.
ID C307_DROME
AC Q9VRM7;
DT 01-OCT-2000 (Rel. 40, Created)
DT 01-OCT-2000 (Rel. 40, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE PROBABLE CYTOCHROME P450 307A1 (EC 1.14.-.-) (CYPCCCVI1A1).
GN CYP307A1 OR CG10594.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Prterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
ON NCBI_TaxID=7221;
RX [1]
SEQUENCE FROM N.A.
RP STRAIN=BERKELEY;
RC MEDLINE=20196006; PubMed=107311132;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Vandell M.D., Zhang Q., Chen L.X.

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Db 254 WLFPYQHLNKKI-INNS--STIRGFI-----MERIIRHRELSVDL 291
QY 145 -----TLQLLNSK-IKKOTLVTVCSGVSKNIYQNLQSOFLHLYQVNSTISVR 193
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 292 DEPDRTFDALLKLEDKQVSRNTIIFMLEDFIGGHSVGNLVMVLVLAIAKNVDIGRR 351
QY 194 VD-----NQFYVNTNTEP--LDNVLSVFLYSSS 219
      : : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 352 IQEBIDAIIEENRSINLLDMNAMPYTMATIFEVLYSSS 391

RESULT 11
FASL_HUMAN
ID FASL_HUMAN STANDARD; PRT: 281 AA.
AC P48023;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (AFTL).
GN TNFSF6 OR APTLIG1 OR FASL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBL_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95105731; PubMed=7528780;
RA Alderson M.;
RT "Fas ligand mediates activation-induced cell death in human T
  lymphocytes.";
RL J. Exp. Med. 181:71-77(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95127560; PubMed=7826947;
RA Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;
RT "Human Fas ligand: gene structure, chromosomal location and species
  specificity.";
RL Int. Immunol. 6:1567-1574(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX Schaeetzlein C.E., Poehlmann R., Philippsen P., Eibel H.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=95071350; PubMed=7980502;
RA Mita E., Hayashi N., Iio S., Takehara T., Hijioka T., Kasahara A.,
RA Fusanoto H., Kamada T.;
RT "Role of Fas ligand in apoptosis induced by hepatitis C virus
  infection.";
RL Biochem. Biophys. Res. Commun. 204:468-474(1994).
RN [5]
RP SEQUENCE FROM N.A.
RA Wilkinson J.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Blood;
RA Matsumura M., Nakanishi Y., Ohba Y.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases
CC -1- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
  TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
  CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
  FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
  PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
  T CELLS, OR BOTH.
CC -1- SUBUNIT: HOMOTRIMER (PROBABLE).
CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
  INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
  SURFACE.
CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
-----
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between the Swiss Institute of Bioinformatics and the EMBL outstation

```

RESULT	13	AMPN_MOUSE	AMPN_HUMAN
ID	AC	P97444	
DT	DT	01-NOV-2000	
DT	DT	01-NOV-2000	
DT	DT	01-NOV-2000	
DE	DE	AMINO-TERMINUS	
DE	DE	(P161)	
GN	GN	ANPEP	
OS	OS	Mus mus	
OC	OC	Eukaryota	
OC	OC	Mammalia	
OC	OC	NCBI_	
OC	OC	[1]	
RP	RP	SEQUENCE	
RA	RA	MEDLINE	
RA	RA	Chen et al	
RT	RT	"p161"	
RT	RT	macrophage	
RT	RT	J. Immunol.	
CC	CC	-i-	
CC	CC	-i-	
CC	CC	-i-	





```
DR PROSITE: PS00251; TNF_1; 1.  
DR PROSITE: PS50049; TNF_2; 1.  
KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.  
FT PROPEP 1 77  
FT CHAIN 78 234 TUMOR NECROSIS FACTOR.  
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
FT DISULFID 146 178 BY SIMILARITY.  
FT CARBOHYD 96 96 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CONFLICT 63 63 MISSING (IN REF. 1).  
SQ SEQUENCE 234 AA; 25536 MW; 4BCF8CCAB7956B88 CRC64;  
  
Query Match 7.2%; Score 82; DB 1; Length 234;  
Best Local Similarity 23.6%; Pred. No. 1.8;  
Matches 47; Conservative 39; Mismatches 89; Indels 24; Gaps 8;  
  
Qy 22 SRSYFYLSTALVCLVAVAILVLVQVKDSTPNTTEKAPLKGKNCSEDLFCTLKST-- 79  
Db 27 SRSCWCLSLFSP--LLVAGATTFLCLLHFGVIGPQREQSP-AGPSFNRLPVQTLRSSQ 83  
  
Qy 80 -PSKSWAYLQVSKHLNNTKLSWNEDGT----IHGLIYQDGNLIVPGLYFIYVCOQL 134  
Db 84 ASNNKPVAVH-VANISAPGOLRWGDSYANALMANGVELKDNLVPTDGLYLIYSQVLF 142  
  
Qy 135 VQ-CSNHSVDLTQLLINSKIKKQTLVTVCES-----GVQSKNIYQNLSQLLH 182  
Db 143 GHGCPSTPLFLT-HTISRAVSYQTKVNLISAISKPSCHRETLEGAERAKPWYEPIYGGVF 201  
  
Qy 183 YLOVNSTISVRVDNQYVD 201  
Db 202 QLEKGRDLSAEINLPYLD 220  
  
RESULT 15  
TNFA_CANFA  
ID TNFA_CANFA STANDARD; PRT; 233 AA.  
AC PS1742; Q28339;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).  
GN TNF OR TNFA.  
OS Canis familiaris (Dog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
OX NCBI_TaxID=9615;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Fiers W., Beernaert M.;  
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Zucker K., Lu P., Fuller L., Asthana D., Esquenazi V., Miller J.;  
RT "Cloning and expression of the cDNA for canine tumor necrosis  
RT factor-alpha in E. coli";  
RL Lymphokine Res. 13:191-196(1994).  
RN [3]  
RP SEQUENCE OF 74-205 FROM N.A.  
RC STRAIN-BEAGLE; TISSUE=Blood;  
RA Gilmore W.H., Carter S.D., Bennett M., Barnes A., Kelly D.F.;  
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.  
CC -I- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE  
CC WITH A WIDE VARIETY OF FUNCTIONS; IT CAN CAUSE CYTOLYSIS OF  
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF  
CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION  
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE  
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN  
CC CONDITIONS.  
CC -I- SUBUNIT: HOMOTRIMER (BY SIMILARITY).  
CC -I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).  
CC -I- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY  
CC PROTEOLYTIC PROCESSING (BY SIMILARITY).  
  
-I- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
CC AND MALNUTRITION.  
CC -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
CC  
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
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CC or send an email to license@isb-sib.ch).  
CC  
CC EMBL; X94932; CAA64403.1; -;  
CC EMBL; S74068; AAB32391.1; -;  
CC EMBL; Z70046; CAA93908.1; -;  
CC HSSP; P01375; ITNF.  
CC InterPro; IPR000478; -;  
CC InterPro; IPR002959; -;  
CC Pfam; PF00229; TNF; 1.  
CC PRINTS; PR01234; TNECROSISFCT.  
CC PRINTS; PR01235; TNFALPHA.  
CC PROSITE; PS00251; TNF_1; 1.  
CC PROSITE; PS50049; TNF_2; 1.  
CC Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.  
FT PROPEP 1 76 POTENTIAL.  
FT CHAIN 77 233 TUMOR NECROSIS FACTOR.  
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
FT DISULFID 145 177 BY SIMILARITY.  
FT CONFLICT 59 60 QR -> PE (IN REF. 2).  
FT CONFLICT 66 66 G -> C (IN REF. 2).  
FT CONFLICT 74 74 A -> V (IN REF. 3).  
FT CONFLICT 111 111 A -> D (IN REF. 2).  
FT CONFLICT 116 116 G -> D (IN REF. 2).  
FT CONFLICT 134 135 IY -> DS (IN REF. 2).  
SQ SEQUENCE 233 AA; 25447 MW; 7B2568FBC8B25340 CRC64;  
  
Query Match 7.1%; Score 81.5; DB 1; Length 233;  
Best Local Similarity 23.6%; Pred. No. 2;  
Matches 48; Conservative 32; Mismatches 90; Indels 33; Gaps 9;  
  
Qy 22 SRSYFYLSTALVCLVAVAILVLVQVKDSTPNTTEKAPLKGKNCSEDLFCTLK 77  
Db 27 SRRCFCLSLFSFLVAVAGATTFLCLLHFGVIGPQRELPN-----GLQLISPLAQTVK 78  
  
Qy 78 S----TPSKSWAYLQVSKHLNNTKLSWNEDGT-----IHGLIYQDGNLIVPGLYFIYVCO 130  
Db 79 SSRTPSDKPVAVHVAANPEAG-OLWLSRRANALLANGVELTDNLQVLIVPSDGLYLIYSQ 137  
  
Qy 131 LOFLVQ-CSNHSVDLTQLLINSKIKKQTLVTV-----CE-----SQVQSKNIYQNL 178  
Db 138 VLKPGGCGPSTHVLTT-HTISRAVSYQTKVNLISAISKPSQRETPTGTEAKPWYEPIYL 196  
  
Qy 179 FLHLHYQVNSTISVRVDNQYVD 201  
Db 197 GGVFQLEKGRDLSAEINLPYLD 219  
  
Search completed: September 5, 2001, 10:29:52  
Job time: 397 sec
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2001, 10:23:51 ; Search time 31.97 Seconds  
(without alignments)  
524.191 Million cell updates/sec

Title: US-09-628-126-19  
Perfect score: 1141  
Sequence: 1 MQVPGSVASPRWRS.....DTNTFPLDNVLSFLYSSD 220

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_68:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1141	100.0	239	2 A40710	CD30 ligand - mous
2	814.5	71.4	234	2 A40710	CD30 ligand - huma
3	109	9.6	279	2 A53062	Fas ligand - mouse
4	91	8.0	278	2 A49266	Fas ligand - rat
5	89.5	7.8	401	2 S74767	hypothetical prote
6	88.5	7.8	309	2 I53384	4-1BB ligand - mou
7	87.5	7.7	235	2 I54490	tumor necrosis fac
8	87	7.6	2013	2 C71610	probable membrane
9	86.5	7.6	2195	2 S61103	SEC16 protein - ye
10	86	7.5	674	2 S61181	hypothetical prote
11	85.5	7.5	994	2 H96510	probable disease r
12	84.5	7.4	884	2 T02731	serine/threonine-s
13	84	7.4	281	2 I38707	Fas ligand - human
14	84	7.4	1110	2 F84547	probable disease r
15	82	7.2	234	1 JH0529	tumor necrosis fac
16	81.5	7.1	304	2 T27593	hypothetical prote
17	81.5	7.1	304	2 T27594	hypothetical prote
18	81	7.1	866	2 T10587	serine/threonine-s
19	80.5	7.1	344	2 T05104	hypothetical prote
20	80	7.0	165	2 H64460	hypothetical prote
21	80	7.0	369	2 S77028	protein kinase, 41
22	79.5	7.0	889	2 T45691	receptor-like prot
23	79	6.9	851	2 S67285	NUD1 protein - yea
24	78.5	6.9	234	1 JQ1344	tumor necrosis fac
25	78.5	6.9	235	2 JU0029	tumor necrosis fac
26	78.5	6.9	1150	2 S49956	probable membrane
27	78	6.8	427	2 T40064	hypothetical prote
28	78	6.8	616	2 T32131	hypothetical prote
29	78	6.8	859	1 VCLJMN	env polyprotein pr

30	77.5	6.8	463	2 S37962	probable purine nu
31	77.5	6.8	1583	2 S59644	sister chromatid c
32	77	6.7	428	2 T48284	hypothetical prote
33	77	6.7	568	2 T20421	hypothetical prote
34	77	6.7	769	2 T39089	hypothetical prote
35	77	6.7	795	2 H84944	phenylalanine--L-RN
36	76.5	6.7	345	2 S03199	opioid-binding pro
37	76.5	6.7	1083	2 A38919	hypothetical prote
38	76.5	6.7	1223	2 T17345	hypothetical prote
39	76	6.7	205	2 H71639	NADH dehydrogenase
40	76	6.7	665	2 T06082	protein kinase hom
41	76	6.7	1313	2 G82887	hypothetical prote
42	75.5	6.6	208	2 B86877	ABC transporter At
43	75.5	6.6	251	2 T25121	hypothetical prote
44	75.5	6.6	303	2 T25114	hypothetical prote
45	75.5	6.6	659	2 T49277	hypothetical prote

ALIGNMENTS

RESULT 1  
B40710  
CD30 ligand - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 05-Nov-1999  
C:Accession: B40710  
R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, Cell 73, 1349-1360, 1993  
A:Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de  
A:Reference number: A40710; MUID:93313964  
A:Accession: B40710  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-239 <SMI>  
A:Cross-references: GB:L09754; NID:g349288; PIDN:AAA74595.1; PID:g349289  
C:Keywords: cytokine receptor; membrane protein; surface antigen

Query Match	100.0%	Score 1141;	DB 2;	Length 239;
Best Local Similarity	100.0%	Pred. No. 1.8e-96;		
Matches 220;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MQVPGSVASPRWRSRSFYLSLTALVCLVAVAILVLVVKKSDPTNTTEK	60	
Db	20	MQVPGSVASPRWRSRSFYLSLTALVCLVAVAILVLVVKKSDPTNTTEK	79	
Qy	61	APLGGGNCSEDLFCTLKSTPSKKSWAYLQVSKHLNNTKLSWNEDGTIHLIYQDGNLIQV	120	
Db	80	APLGGGNCSEDLFCTLKSTPSKKSWAYLQVSKHLNNTKLSWNEDGTIHLIYQDGNLIQV	139	
Qy	121	PPGLYFVLCQLQFLVQCSNHSVDLTLQLLNSKIKQTLVTVCESGVOSKNLYQNLSQFL	180	
Db	140	PPGLYFVLCQLQFLVQCSNHSVDLTLQLLNSKIKQTLVTVCESGVOSKNLYQNLSQFL	199	
Qy	181	LHYLQVNSTISVRVDNFQYVDNTFPLDNVLSFLYSSD	220	
Db	200	LHYLQVNSTISVRVDNFQYVDNTFPLDNVLSFLYSSD	239	

RESULT 2  
A40710  
CD30 ligand - human  
C:Species: Homo sapiens (man)  
C:Date: 03-May-1994 #sequence\_revision 03-May-1994 #text\_change 21-Jul-2000  
C:Accession: A40710  
R:Smith, C.A.; Gruss, H.J.; Davis, T.; Anderson, D.; Farrah, T.; Baker, E.; Sutherland, M.; Falk, B.; Gimpel, S.; Gillis, S.; Din, W.S.; Goodwin, R.G.; Armitage, Cell 73, 1349-1360, 1993  
A:Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de  
A:Reference number: A40710; MUID:93313964  
A:Accession: A40710

A;reference number: A49266; MOID:94084/92  
A;Accession: A49266

A,Reference number: I53384; MUID:94009225  
A,Accession: I53384

C;Accession: C71610  
R.; Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.  
H.; Perteau, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith,  
Science 282, 1126-1132, 1998  
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.  
A;Reference number: A71600; MUID:99021743  
A;Accession: C71610  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-2013 <GAR>  
A;Cross-references: GB:AE001406; GB:AE001362; NID:g3845230; PIDN:AAC71912.1; PID:g384  
A;Experimental source: clone 3D7  
C;Genetics:  
A;Gene: PF0615c

Query Match 7.6%; Score 87; DB 2; Length 2013;  
Best Local Similarity 23.9%; Pred. No. 18;  
Matches 34; Conservative 31; Mismatches 49; Indels 28; Gaps 7;

Qy 69 SEDLFTLKSTPSKSWAYLVQSKHLNNTKLWNEDGTHGLIYQGNLIQVPGPLYFIY 128  
| : : | | | | : : : | : : : | : : : | : : : | : : : | : : :  
Db 16 SDNIFCLKD-----GYICFNNLLN-----NEKKYLITCSQDSGYAQY---YFDV 59

Qy 129 COLQFLVOCSNHVSVDLPQLLI-----NSKKTKQTLTVCESGVOSKNIYNLSQFL-- 181  
| : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :  
Db 60 VKCRYEKEEDCKNMNTIMLLQNENKKIKETCYI---KNVVTKNIYHTL--FLWINK 114

Qy 182 HYLOVNSTISVRVDNFQYVDTN 203  
| : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :  
Db 115 HYHNILCSLFENNSSFELLMTN 136

RESULT 9  
S61103  
SEC16 protein - yeast (Saccharomyces cerevisiae)  
N;Alternate names: protein LPFlw; protein YPL085w  
C;Species: Saccharomyces cerevisiae  
C;Date: 23-Feb-1996 #sequence\_revision 01-Mar-1996 #text\_change 06-Feb-1998  
C;Accession: S61103  
R;Hall, J.; Ahmed, A.; Bussey, H.; Fortin, N.; Friesen, J.D.; Storms, R.K.; Vo, D.H.;  
submitted to the EMBL Data Library, August 1995  
A;Description: The sequence of Saccharomyces cerevisiae chromosome XVI left arm.  
A;Reference number: S59677  
A;Accession: S61103  
A;Molecule type: DNA  
A;Residues: 1-2195 <HAL>  
A;Cross-references: EMBL:U41849; NID:g1147608; PID:g1147609; MIPS:YPL085w  
C;Genetics:  
A;Gene: SGD:SEC16  
A;Cross-references: SGD:S0006006; MIPS:YPL085w  
A;Map position: 16L  
C;Keywords: transmembrane protein  
F;1198-1214/Domain: transmembrane #status predicted <TM1>  
F;1250-1266/Domain: transmembrane #status predicted <TM2>

Query Match 7.6%; Score 86.5; DB 2; Length 2195;  
Best Local Similarity 20.9%; Pred. No. 22;  
Matches 53; Conservative 39; Mismatches 87; Indels 75; Gaps 13;

Qy 7 SVASPFWRSTRP-----WRSTSRSYF-----YLTSTALVCLWA 39  
| | | | : : : | : : : | : : : | : : : | : : : | : : :  
Db 970 SVAPROENNPDKIDNEALLRRQPPIFHSAANKVAVVPDPDSQMYSSSIQVEIKV 1029

Qy 40 VAILVLVVKKK---STPNTEKAPLKGNCSDLEFCTLKTSFKS-----WAYLQV 90  
| : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :  
Db 1030 TPI--DQIIKPNMLKSPFGPLGSAKLKKDL/KWMETTIKSISENESDWTMTIWOLLE 1087

Qy 91 SKHLNNTKLSWNEDGTHGLIYQGNLIY-----QFPGLY--FIVCOQLF--VQ 136  
| : : | : : : | : : : | : : : | : : : | : : : | : : : | : : :  
Db 1088 KL---NDKVNNK-----NTSKULYSDELMIYLSQFPFGNGDMIPNAYRLDINCOMRVLAFLQ 1141

RESULT 11  
H96510  
probable disease resistance protein [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: H96510  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719  
A:Accession: H96510  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-994 <STO>  
A:Cross-references: GB:AE005173; NID:g11321768; PTDN:AAG34245.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: F2G19.6  
A:Map position: 1

j

## RESULT 13

I38707  
Fas ligand - human  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 21-Jul-2000  
C:Accession: I38707; J02340; S57565; I38554  
R: Takahashi, T.; Tanaka, M.; Inazawa, J.; Abe, T.; Suda, T.; Nagata, S.  
Int. Immunol. 6, 1567-1574, 1994  
A:Title: Human Fas ligand: gene structure, chromosomal location and species specificity.  
A:Reference number: I38707; MUID:95127560  
A:Accession: I38707  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-281 <RES>  
A:Cross-references: EMBL:U11821; NID:9595430; PIDN:AAC50124.1; PID:9595431  
R: Mita, E.; Hayashi, N.; Iio, S.; Takehara, T.; Hijioaka, T.; Kasahara, A.; Fusamoto, H.;  
Biochem. Biophys. Res. Commun. 204, 468-474, 1994  
A:Title: Role of Fas ligand in apoptosis induced by hepatitis C virus infection.  
A:Reference number: J02340; MUID:95071350  
A:Accession: J02340  
A:Molecule type: DNA  
A:Residues: 1-281 <MIT>  
A:Cross-references: GB:D38122; DBJ:D29820; NID:9601892; PIDN:BAA07320.1; PID:g1369902  
R: Schatzlein, C.E.  
submitted to the EMBL Data Library, June 1995  
A:Reference number: S57565  
A:Accession: S57565  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-281 <SCH>  
A:Cross-references: EMBL:X89102; NID:9887455; PID:9887456  
R: Alderson, M.R.; Tough, T.W.; Davis-Smith, T.; Braddy, S.; Falk, B.; Schooley, K.A.; Go  
J. Exp. Med. 181, 71-77, 1995  
A:Title: Fas ligand mediates activation-induced cell death in human T lymphocytes.  
A:Reference number: I38554; MUID:95105731  
A:Accession: I38554  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-281 <RE2>  
A:Cross-references: EMBL:U08137; NID:g624627; PIDN:AAC50071.1; PID:g624628  
C:Genetics:  
A:Gene: FasL  
A:Introns: 151/1; 116/3  
C:Keywords: glycoprotein; transmembrane protein  
F:80-102/Domain: transmembrane #status predicted <TMM>  
F:76,184,250,260/Binding site: carbohydrate (Asn) (covalent) #status predicted

## Query Match 7.4%; Score 84; DB 2; Length 281;

Best Local Similarity 20.3%; Pred. No. 3.3;  
Matches 42; Conservative 36; Mismatches 65; Indels 64; Gaps 9;

QY 34 VCLVAVAIILVLV-----QKKDSTPNTTEKAPLKGNGCEDLFC 74  
DB 81 LCLLVNFFWVVALVGLGLGMFOLHQLKELARESTSQMHTASSLEKQIGHPS-----135  
QY 75 TLKSTPSKSSW---AYLQVSKHLNNTKLSWNEGTI---HGLIYQDGNLIVQFPLGYFIV 128  
DB 136 ---PPPEKELRKAHLTKGNSRSRMPLEWEDTYGIVLLSGVKYKKGGLVNETGLYFVY 192  
QY 129 COLQFLVQ-CSN-----HSVDLTQLQLNSK-----IKKQTLVTVCSG-----166  
DB 193 SKVYFRGQSCNNPLSLSHK-----YMRNSKYPDQLVNMCKMMSYCTTGQMWARSVSLGA 247  
QY 167 ----VQSKNIYQNLSFLHLYQVNST 189

DB 248 VFNLTSADHLVNVSELSLVNFEQSOT 274

## RESULT 14

F84547  
probable disease resistance protein [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C:Accession: F84547  
R: Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487  
A:Accession: F84547  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1110 <STO>  
A:Cross-references: GB:AE002093; NID:g6598362; PIDN:AAF18600.1; GSPDB:GN00139  
C:Genetics:  
A:Gene: At2g17060  
A:Map position: 2

## Query Match 7.4%; Score 84; DB 2; Length 1110;

Best Local Similarity 22.7%; Pred. No. 16;  
Matches 44; Conservative 36; Mismatches 66; Indels 48; Gaps 10;

QY 27 YLSTTALVCLVAV---AIIILV-----LVVQKKDSTPNTTEKAPLKGNGCEDLFC 76  
DB 680 YLQTAIKCIPTSIENLOKLIIILLDKCEVIVSLPDLGNLRSLOELILSGCSK-----L 734  
QY 77 KSTPSKSWAYLQVSKHLNNTKLSWNEGTIHLIYQDGNLIVQFPLGYFIVCOLQFLVQ 136  
DB 735 KFFPELK-----ETMKSIK-----ILLDDGTAKQMPIL---LQC-----IQ 768  
QY 137 CSNHSV-DLTQLLINSKIKKOTLVTVCSGVQSKNIYQNLSQ-FLHLYQVNS-----T 189  
DB 769 SOGHSVANKTLPNSISDYLYPSSLISLCLSGNDIESLHANSIQLYHLKWLKLNKCKLKS 828  
QY 190 ISVRVDNFQYVDN 203  
DB 829 VSLPPNLKCLDAH 842

## RESULT 15

JH0529

tumor necrosis factor alpha precursor - sheep

N:Alternate names: cachectin; TNF alpha

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000

C:Accession: JH0529; S48118; S13114; S20661

R:Green, I.R.; Sargan, D.R.

Gene 109, 203-210, 1991

A:Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems wi

A:Reference number: JH0529; MUID:92112044

A:Accession: JH0529

A:Molecule type: mRNA

A:Residues: 1-234 <GRE>

A:Cross-references: EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406

A:Experimental source: alveolar macrophage

R:Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E.

Immunol. Cell Biol. 69, 273-283, 1991

A:Title: Molecular cloning, expression and characterization of ovine TNF-alpha.

A:Reference number: S48118; MUID:92155784

A:Accession: S48118

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-234 <NAS>

A:Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807

R:Young, A.J.; Hay, J.B.; Chan, J.Y.C.

Nucleic Acids Res. 18, 6723, 1990

A:Title: Primary structure of ovine tumor necrosis factor alpha cDNA.

A:Reference number: S13114; MUID:91067496

A:Accession: S13114

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-62,64-234 <YOU>

A:Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404

A:Note: comparison with the introns of homologous sequences suggest that this is probably  
C:Superfamily: tumor necrosis factor  
F:1-77/Domain: propeptide #status predicted <PRO>  
F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>  
F:20/Binding site: myristate (Lys) (covalent) #status predicted  
F:82/Binding site: carbohydrate (Ser) (covalent) #status predicted  
F:96/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:146-178/Disulfide bonds: #status predicted

Query Match	7.2%	Score 82;	DB 1;	Length 234;
Best Local Similarity	23.6%	Pred. No. 4;		
Matches 47;	Conservative 39;	Mismatches 89;	Indels 24;	Gaps 8;
Qy 22	SRSYFYLETTALVCLVAVAIILVLVVKKDSPTNTTEKAPLKGGNCSEDLFCTLKST--	79		
Db 27	SRSCWCLSLFSP--LLVAGATTFLCLLHFGVIGPQREEQSP-AGPSFNRPVQTLRSSQ	83		
Qy 80	-PSKKSWAYLVQVSKHLNNTKLSWNEDGT----IHGLIYQDGNLIVQPGLYFIVCOLQFL	134		
Db 84	ASNKKPVAHV-VANISAPQLRWGDSYANALMANGVELKDNLVPTDGLYLYSQVLF	142		
Qy 135	VQ-CSNHSVDLTLQLLINSKIKKQTLVTVCES-----GVOSKNIYQNLSQLH	182		
Db 143	GHGCPSTPLFLT-HTISRIAVSYQTKVNILSAIKSPCHRETLEGAEPWYPIYQGGVF	201		
Qy 183	YLOVNSTISVRVDNFQYVD	201		
Db 202	QLEKGRLSAEINLPEYLD	220		

Search completed: September 5, 2001, 10:23:52  
Job time: 122 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2001, 10:23:10 ; Search time 25.09 Seconds  
(without alignments)  
180.545 Million cell updates/sec

Title: US-09-628-126-19  
Perfect score: 1141  
Sequence: 1 MQVPGSVASWRTRPWS.....DTNTPPLDNVLVSFLYSSD 220

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents:AA:\*  
1: /cgn2.6/ptodata/2/iaa/5A\_COMB.pep.\*  
2: /cgn2.6/ptodata/2/iaa/5B\_COMB.pep.\*  
3: /cgn2.6/ptodata/2/iaa/6A\_COMB.pep.\*  
4: /cgn2.6/ptodata/2/iaa/6B\_COMB.pep.\*  
5: /cgn2.6/ptodata/2/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2.6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1141	100.0	220	1	US-08-225-989-19
2	1141	100.0	220	1	US-08-570-923-19
3	1141	100.0	220	1	US-08-580-014-19
4	1141	100.0	220	4	US-09-079-785-19
5	1141	100.0	239	1	US-08-225-989-6
6	1141	100.0	239	1	US-08-570-923-6
7	1141	100.0	239	1	US-08-580-014-6
8	1141	100.0	239	4	US-09-079-785-6
9	814.5	71.4	215	1	US-08-225-989-23
10	814.5	71.4	215	1	US-08-570-923-23
11	814.5	71.4	215	4	US-08-580-014-23
12	814.5	71.4	215	4	US-09-079-785-23
13	814.5	71.4	234	1	US-08-225-989-8
14	814.5	71.4	234	1	US-08-570-923-8
15	814.5	71.4	234	1	US-08-580-014-8
16	814.5	71.4	234	4	US-09-079-785-8
17	685	60.0	130	1	US-08-225-989-21
18	685	60.0	130	1	US-08-570-923-21
19	685	60.0	130	1	US-08-580-014-21
20	685	60.0	130	4	US-09-079-785-21
21	624	54.7	148	3	US-08-584-031-12
22	388.5	34.0	125	1	US-08-225-989-20
23	388.5	34.0	125	1	US-08-570-923-20
24	388.5	34.0	125	1	US-08-580-014-20
25	388.5	34.0	125	4	US-09-079-785-20
26	229	20.1	52	4	US-09-369-494-17
27	104	9.1	279	5	PCT-US95-00362-5

Sequence 2, Appli  
Sequence 6, Appli  
Sequence 6, Appli  
Sequence 2, Appli  
Sequence 2, Appli  
Sequence 25, Appli  
Sequence 3, Appli  
Sequence 2, Appli  
Sequence 16, Appli  
Sequence 140, Appli  
Sequence 137, Appli  
Sequence 143, Appli  
Sequence 4, Appli  
Sequence 4, Appli  
Sequence 8, Appli  
Sequence 10, Appli  
Sequence 10, Appli

US-08-225-989-19  
; Sequence 19, Application US/08225989  
; Patent No. 5480981  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jürgen  
; TITLE OF INVENTION: NO. 5480981el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644

## ALIGNMENTS

RESULT 1  
US-08-225-989-19  
; Sequence 19, Application US/08225989  
; Patent No. 5480981  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jürgen  
; TITLE OF INVENTION: NO. 5480981el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644

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; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 220 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-225-989-19

Query Match          100.0%; Score 1141; DB 1; Length 220;
Best Local Similarity 100.0%; Pred. No. 2.1e-110;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQVQPGSVASPRWSTPRWSTRSFYLSYFVLTALVCLVAVAILLVVQVKDSTPNTTEK 60
DB 1 MQVQPGSVASPRWSTPRWSTRSFYLSYFVLTALVCLVAVAILLVVQVKDSTPNTTEK 60
QY 61 APLKGGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 120
DB 61 APLKGGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 120
QY 121 FPGLYFIVCOLQFLVQCSNHSVDLTQLLLINSKIKKQTLVTVCSGVQSKNIYQNLISOFL 180
DB 121 FPGLYFIVCOLQFLVQCSNHSVDLTQLLLINSKIKKQTLVTVCSGVQSKNIYQNLISOFL 180
QY 181 LHYLQVNSTISVRVDNFQYVDNTFPLDNVLSVFLYSSSD 220
DB 181 LHYLQVNSTISVRVDNFQYVDNTFPLDNVLSVFLYSSSD 220

RESULT 2
US-08-570-923-19
; Sequence 19, Application US/08570923
; Patent No. 5677430
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,923
; FILING DATE: 12-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
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; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 220 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-570-923-19

Query Match          100.0%; Score 1141; DB 1; Length 220;
Best Local Similarity 100.0%; Pred. No. 2.1e-110;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQVQPGSVASPRWSTPRWSTRSFYLSYFVLTALVCLVAVAILLVVQVKDSTPNTTEK 60
DB 1 MQVQPGSVASPRWSTPRWSTRSFYLSYFVLTALVCLVAVAILLVVQVKDSTPNTTEK 60
QY 61 APLKGGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 120
DB 61 APLKGGNCSEDLFCTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 120
QY 121 FPGLYFIVCOLQFLVQCSNHSVDLTQLLLINSKIKKQTLVTVCSGVQSKNIYQNLISOFL 180
DB 121 FPGLYFIVCOLQFLVQCSNHSVDLTQLLLINSKIKKQTLVTVCSGVQSKNIYQNLISOFL 180
QY 181 LHYLQVNSTISVRVDNFQYVDNTFPLDNVLSVFLYSSSD 220
DB 181 LHYLQVNSTISVRVDNFQYVDNTFPLDNVLSVFLYSSSD 220

RESULT 3
US-08-580-014-19
; Sequence 19, Application US/08580014
; Patent No. 5753203
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,014
; FILING DATE: 20-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
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; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-580-014-19

Query Match 100.0%; Score 1141; DB 1; Length 220;
Best Local Similarity 100.0%; Pred. No. 2.le-110;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MQVPGSVASPRSTRPWRSTSRYSFYLTALVCLVAVAILLVVQKKDSTPNTTEK 60

QY 61 APLKGGNCSEDLFCTLKSTPSKKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQ 120
DB 61 APLKGGNCSEDLFCTLKSTPSKKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQ 120

QY 121 FPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVTVCSGVQSKNIYQNLSQFL 180
DB 121 FPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVTVCSGVQSKNIYQNLSQFL 180

QY 181 LHLYQVNSTISVRVDNFQYVDTNTPFLDNVLSVFLYSSD 220
DB 181 LHLYQVNSTISVRVDNFQYVDTNTPFLDNVLSVFLYSSD 220

RESULT 4
US-09-785-19
; Sequence 19, Application US/09079785
; Patent No. 6143869
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 6143869el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
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; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,785
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 220 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-079-785-19

Query Match 100.0%; Score 1141; DB 4; Length 220;
Best Local Similarity 100.0%; Pred. No. 2.le-110;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MQVPGSVASPRSTRPWRSTSRYSFYLTALVCLVAVAILLVVQKKDSTPNTTEK 60
DB 1 MQVPGSVASPRSTRPWRSTSRYSFYLTALVCLVAVAILLVVQKKDSTPNTTEK 60

QY 61 APLKGGNCSEDLFCTLKSTPSKKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQ 120
DB 61 APLKGGNCSEDLFCTLKSTPSKKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQ 120

QY 121 FPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVTVCSGVQSKNIYQNLSQFL 180
DB 121 FPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVTVCSGVQSKNIYQNLSQFL 180

QY 181 LHLYQVNSTISVRVDNFQYVDTNTPFLDNVLSVFLYSSD 220
DB 181 LHLYQVNSTISVRVDNFQYVDTNTPFLDNVLSVFLYSSD 220

RESULT 5
US-08-225-989-6
; Sequence 6, Application US/08225989
; Patent No. 5480981
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
```

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; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-225-989-6

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Query Match 100.0%; Score 1141; DB 1; Length 239;
Best Local Similarity 100.0%; Pred. No. 2.4e-110;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MQVPGSVASPRSTRPWRSTRSRFYLLSTALVCLVAVAILLVVQKDKSTPTTEK 60
Db 20 MQVPGSVASPRSTRPWRSTRSRFYLLSTALVCLVAVAILLVVQKDKSTPTTEK 79
QY 61 APLKGGNCSEDLFTCLKSTPKSKSWAYLOVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 120
Db 80 APLKGGNCSEDLFTCLKSTPKSKSWAYLOVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 139
QY 121 FPGLYFIVCQLOFLVQCSNHSVDLTQLLLINSKIKKQTLVTVCSGVQSKNIYONLSQFL 180
Db 140 FPGLYFIVCQLOFLVQCSNHSVDLTQLLLINSKIKKQTLVTVCSGVQSKNIYONLSQFL 199
QY 181 LHYLVQNSTISVRVDNQYDNTFTPLDNLVLSFLYSSD 220
Db 200 LHYLVQNSTISVRVDNQYDNTFTPLDNLVLSFLYSSD 239

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RESULT 6
US-08-570-923-6
; Sequence 6, Application US/08570923
; Patent No. 5677430

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; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,923
; FILING DATE: 12-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-570-923-6

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Query Match 100.0%; Score 1141; DB 1; Length 239;
Best Local Similarity 100.0%; Pred. No. 2.4e-110;
Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MQVPGSVASPRSTRPWRSTRSRFYLLSTALVCLVAVAILLVVQKDKSTPTTEK 60
Db 20 MQVPGSVASPRSTRPWRSTRSRFYLLSTALVCLVAVAILLVVQKDKSTPTTEK 79
QY 61 APLKGGNCSEDLFTCLKSTPKSKSWAYLOVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 120
Db 80 APLKGGNCSEDLFTCLKSTPKSKSWAYLOVSKHLNNTKLSWNEDGTIHGLIYQDGNLIVQ 139
QY 121 FPGLYFIVCQLOFLVQCSNHSVDLTQLLLINSKIKKQTLVTVCSGVQSKNIYONLSQFL 180
Db 140 FPGLYFIVCQLOFLVQCSNHSVDLTQLLLINSKIKKQTLVTVCSGVQSKNIYONLSQFL 199

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QY 181 LHYLQVNSTISVRVDNFQYVDNTETPLDNVLSVFLYSSD 220  
 |||||  
 Db 200 LHYLQVNSTISVRVDNFQYVDNTETPLDNVLSVFLYSSD 239

RESULT 7  
 US-08-580-014-6  
 ; Sequence 6, Application US/08580014  
 ; Patent No. 5753203  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Goodwin, Raymond G.  
 ; APPLICANT: Smith, Craig A.  
 ; APPLICANT: Armitage, Richard J.  
 ; APPLICANT: Gruss, Hans-Jürgen  
 ; TITLE OF INVENTION: No. 5753203el  
 ;

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Query Match      100.0%; Score 1141; DB 1; Length 239;
Best Local Similarity 100.0%; Pred. No. 2.4e-110;
Matches 220: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      20  MQVPGSVASPWSTRPWRSTSRKSYFLSTTALVCLVAVAILLVLVOKDSTPTTEK 79
Qy      61  APLKGGNCSEDLFCTLKSTPSKKSWAYLVQSKHLNNTKLSWNEDGTIHGLIYQDGNLIQ 120
Db      80  APLKGGNCSEDLFCTLKSTPSKKSWAYLVQSKHLNNTKLSWNEDGTIHGLIYQDGNLIQ 139
Qy     121  FPGLYFTVCOQLFVOCNSHNSVDLTQLQLINSKIKKQTLVTVCESGVQSKNIYQNLSQFL 180
Db     140  FPGLYFTVCOQLFVOCNSHNSVDLTQLQLINSKIKKQTLVTVCESGVQSKNIYQNLSQFL 199
Qy     181  LHLYOVNSTISVRVDFNQYVDTNTFFLDNVLVSFLYSSSD 220
Db     200  LHLYOVNSTISVRVDFNQYVDTNTFFLDNVLVSFLYSSSD 239

RESULT      8
; Sequence 6, Application US/09079785
; Patent No. 6143869
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jürgen
; TITLE OF INVENTION: No. 6143869el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,785
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239 amino acids
; TYPE: amino acid

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;
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-079-785-6

Query Match 100.08; Score 1141; DB 4; Length 239;
Best Local Similarity 100.08; Pred. No. 2.4e-110; Indels 0; Gaps 0;
Matches 220; Conservative 0; Mismatches 0;

Qy 1 MQVPGSVASPRSTRPWRSTSRYSFYLTALVCLVAVAILVVLVQKDSPTNTEK 60
Db 20 MQVPGSVASPRSTRPWRSTSRYSFYLTALVCLVAVAILVVLVQKDSPTNTEK 79

Qy 61 APLKGCNSEDLCFTLKSTPSKSWAYLOVSKHLNNTKLSWNEEDGTIHGLIYODGNLIV 120
Db 80 APLKGCNSEDLCFTLKSTPSKSWAYLOVSKHLNNTKLSWNEEDGTIHGLIYODGNLIV 139

Qy 121 FPLGLFYICQLQFLVQCSNHSVDLTLLQLLNSKIKKQTLVTVCESGVQSKNIYONLSQFL 180
Db 140 FPLGLFYICQLQFLVQCSNHSVDLTLLQLLNSKIKKQTLVTVCESGVQSKNIYONLSQFL 199

Qy 181 LHYLVQNSTISVRVDFNQVDTNTPFDNLVSLVFLYSSSD 220
Db 200 LHYLVQNSTISVRVDFNQVDTNTPFDNLVSLVFLYSSSD 239

RESULT 9
US-08-225-989-23
; Sequence 23, Application US/08225989
; Patent No. 5480981
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
```

```
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-225-989-23

Query Match 71.48; Score 814.5; DB 1; Length 215;
Best Local Similarity 70.68; Pred. No. 1.12e-76;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

Qy 1 MQVPGSVASPRSTRPWRSTSRYSFYLTAL-VCLVAVAILVVLVQKDSPTNTE 59
Db 1 MHVPAGSVAS-----HLGTSTSRYSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPD 54

Qy 60 KAPLKGNCSEDLFCFTLKSTPSKSWAYLOVSKHLNNTKLSWNEEDGTIHGLIYODGNLIV 119
Db 55 NVPLKGCNSEDLLCILKRAPFKASWAYLQVAKHLNNTKLSWNGDGLHGVRYODGNLIV 114

Qy 120 QPFLGYFIVCOLQFLVQCSNHSVDLTLLQLLNSKIKKQTLVTVCESGVQSKNIYONLSQF 179
Db 115 QPFLGYFIVCOLQFLVQCPNNSVDLKLLELLINKHKQALVTVCESGMQTKHVVQNLQSF 174

Qy 180 LHYLVQNSTISVRVDFNQVDTNTPFDNLVSLVFLYSSSD 220
Db 175 LLDYLVQNTTISVNVDTFOYIDTSTFPLENVLSIFLYSNSD 215

RESULT 10
US-08-570-923-23
; Sequence 23, Application US/08570923
; Patent No. 5677430
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/570,923
; FILING DATE: 12-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
```

;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 892,459  
;; FILING DATE: 02-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 889,717  
;; FILING DATE: 26-MAY-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Seese, Kathryn A.  
;; REGISTRATION NUMBER: 32,172  
;; REFERENCE/DOCKET NUMBER: 2804-E  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206)587-0430  
;; TELEFAX: (206)233-0644  
;; TELEX: 756822  
;; INFORMATION FOR SEQ ID NO: 23:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 215 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-570-923-23

Query Match 71.4%; Score 814.5; DB 1; Length 215;  
Best Local Similarity 70.6%; Pred. No. 1.2e-76;  
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;  
Qy 1 MQVPGSVASPRSTRPWRSTRSRYSFYLLSTAL-VCLVAVAILVLVQKDSPTNTTE 59  
Db 1 MHVPAGSVAS-----HLGTTSRYSFYLLTATLALCLVFTVATIMVLVQRTDSIPNSPD 54  
Qy 60 KAPLKGNCSEDLFCTLKSTPSKKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIV 119  
Db 55 NVPLKGGNCSEDLCLILKRAPFKKSWAYLQVAKHLNKTLSWNKDGILHGVRYQDGNLVI 114  
Qy 120 QPGLYFIVCOLQFLVQCSNHSVDLTQLLLINSKIKKQTLVTVCSGVQSKNIYQNLISQF 179  
Db 115 QPGLYFIIICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTVCSGMQTKHYQNLISQF 174  
Qy 180 LLHYLQVNSTISVRVDFQYVDNTFTPLDNLVSFLYSSSD 220  
Db 175 LLDYLQVNTTISVNVDTFTFYIDTSTFPLENLSIFLYSNSD 215

RESULT 11  
US-08-580-014-23  
; Sequence 23, Application US/08580014  
; Patent No. 5753203  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/580,014  
; FILING DATE: 20-DEC-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989

;; FILING DATE: 12 APRIL 1994  
;; APPLICATION NUMBER: US 07/966,775  
;; FILING DATE: 27-OCT-1992  
;; CLASSIFICATION: 530  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 907,224  
;; FILING DATE: 01-JUL-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 899,660  
;; FILING DATE: 15-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 892,459  
;; FILING DATE: 02-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 889,717  
;; FILING DATE: 26-MAY-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Seese, Kathryn A.  
;; REGISTRATION NUMBER: 32,172  
;; REFERENCE/DOCKET NUMBER: 2804-E  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206)587-0430  
;; TELEFAX: (206)233-0644  
;; TELEX: 756822  
;; INFORMATION FOR SEQ ID NO: 23:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 215 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
US-08-580-014-23

Query Match 71.4%; Score 814.5; DB 1; Length 215;  
Best Local Similarity 70.6%; Pred. No. 1.2e-76;  
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;  
Qy 1 MQVPGSVASPRSTRPWRSTRSRYSFYLLSTAL-VCLVAVAILVLVQKDSPTNTTE 59  
Db 1 MHVPAGSVAS-----HLGTTSRYSFYLLTATLALCLVFTVATIMVLVQRTDSIPNSPD 54  
Qy 60 KAPLKGNCSEDLFCTLKSTPSKKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIV 119  
Db 55 NVPLKGGNCSEDLCLILKRAPFKKSWAYLQVAKHLNKTLSWNKDGILHGVRYQDGNLVI 114  
Qy 120 QPGLYFIVCOLQFLVQCSNHSVDLTQLLLINSKIKKQTLVTVCSGVQSKNIYQNLISQF 179  
Db 115 QPGLYFIIICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTVCSGMQTKHYQNLISQF 174  
Qy 180 LLHYLQVNSTISVRVDFQYVDNTFTPLDNLVSFLYSSSD 220  
Db 175 LLDYLQVNTTISVNVDTFTFYIDTSTFPLENLSIFLYSNSD 215

RESULT 12  
US-09-079-785-23  
; Sequence 23, Application US/09079785  
; Patent No. 6143869  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 6143869el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,785
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-079-785-23

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Query Match 71.4%; Score 814.5; DB 4; Length 215;
Best Local Similarity 70.6%; Pred. No. 1.2e-76;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

Qy 1 MQVQPGSVASPRWSTPRWSTSRSYFYLTAL-VCLVAVAILLVQKDKSTPNTTE 59
Db 1 MHVPAGSVAS-----HLGTTSRSYFYLTATLALCLVFTVATIMLVVQRTDSIPNSPD 54

Qy 60 KAPLKGNCSEDLCTLKSTPSKSWAYLQVSKHLNNTKLSNEDGTIHLIYQDGNLIV 119
Db 55 NVPLKGGNCSEDLICILKRAPKSWAYLQVAKHLNNTKLSNKGILHGVRYQDGNLVI 114

Qy 120 QPGLYFIICQLQFLVQCPNNSVDLTKLINSKIKKQTLVTVCSGVSKNIYQNLQSF 179
Db 115 QPGLYFIICQLQFLVQCPNNSVDLTKLINSKIKKQTLVTVCSGVSKNIYQNLQSF 174

Qy 180 LLHYLQVNSTISVRVDFQYVDNTFPDLNVLVSFLYSSSD 220
Db 175 LLDYLVQNTTISVNDTFQYIDTSTFPLENVLVSFLYSSSD 215

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RESULT 13
US-08-225-989-8
; Sequence 8, Application US/08225989
; Patent No. 5480981
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen

```

```

; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 907,224
; FILING DATE: 01-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 899,660
; FILING DATE: 15-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 892,459
; FILING DATE: 02-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-225-989-8

Query Match 71.4%; Score 814.5; DB 1; Length 234;
Best Local Similarity 70.8%; Pred. No. 1.3e-76;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

Qy 1 MQVQPGSVASPRWSTPRWSTSRSYFYLTAL-VCLVAVAILLVQKDKSTPNTTE 59
Db 20 MHVPAGSVAS-----HLGTTSRSYFYLTATLALCLVFTVATIMLVVQRTDSIPNSPD 73

Qy 60 KAPLKGNCSEDLCTLKSTPSKSWAYLQVSKHLNNTKLSNEDGTIHLIYQDGNLIV 119
Db 74 NVPLKGGNCSEDLICILKRAPKSWAYLQVAKHLNNTKLSNKGILHGVRYQDGNLVI 133

Qy 120 QPGLYFIICQLQFLVQCPNNSVDLTKLINSKIKKQTLVTVCSGVSKNIYQNLQSF 179
Db 134 QPGLYFIICQLQFLVQCPNNSVDLTKLINSKIKKQTLVTVCSGVSKNIYQNLQSF 193

Qy 180 LLHYLQVNSTISVRVDFQYVDNTFPDLNVLVSFLYSSSD 220
Db 194 LLDYLVQNTTISVNDTFQYIDTSTFPLENVLVSFLYSSSD 234

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RESULT 14



US-08-570-923-8  
; Sequence 8, Application US/08570923  
; Patent No. 5677430  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/570,923  
; FILING DATE: 12-DEC-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 234 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-570-923-8

Query Match 71.4%; Score 814.5; DB 1; Length 234;  
Best Local Similarity 70.6%; Pred. No. 1.3e-76;  
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;  
QY 1 MQVQGSVAPWRSTPRWSTRSYFLSTAL-VCLVAVAILVLVQKSTPNTTE 59  
Db 20 MHVPAGSVAS-----HLGTSRSYFLTTALCLVETVATIMLVVQRTDSIPNSPD 73  
QY 60 KAPLKGNGCNSEDLCFKLSTPSKSNAYLQVSKHLNKLWNEDGTIHLIYQDGNLIV 119  
Db 74 NVPLKGGNCSDELCLILKRAPFKSNAYLQVAKHLNKLWNKDGILHGVRYQDGNLVI 133

QY 120 QPGLYFTVCOLOFLVQCSNHSVDLTLLINKSKTKOTFLVTVCSGVQSKNIYONLSQF 179  
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QY 180 LLHYLQVNSTISVRVDFNQYVDNTFFPLDNVLSVFLYSSD 220  
Db 194 LLDYLVQVNTTISVNVDTFQYIDTSTFPLENVLSIFLYNSD 234  
RESULT 15  
US-08-580-014-8  
; Sequence 8, Application US/08580014  
; Patent No. 5753203  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/580,014  
; FILING DATE: 20-DEC-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 234 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-580-014-8

Query Match 71.4%; Score 814.5; DB 1; Length 234;  
Best Local Similarity 70.6%; Pred. No. 1.3e-76;

Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

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QY 1  MQVPGSVASPRSTRPWRSTSRSYFYLTAL-VCLWAVAILVLVQKKDSTPNTTE 59
Db 20 MHPAGSVAS-----HLGTTSRSYFYLTATLALCLVFTVATIMVLVQRTDSIPNSPD 73
QY 60 KAPLKGNCSEDLFTLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYODGNLIV 119
Db 74 NVPLKGCNCSEDLCLIKRAPFKKSWAYLQVAKHLNNTKLSWNKDGILHGVRYODGNLVI 133
QY 120 QFFGLYFIYVQLOFLVQCSNHSVDLTILQILLINSKIKKQTLVTVCESGVQSKNIYQNLQF 179
Db 134 QFFGLYFIYVQLOFLVQCPNNSVDLKLLELLINKHIKKQALVTVCESGMQTKHVIYQNLQF 193
QY 180 LLHYLQVNSTISVRVDNFQYVDNTFFLDNVLVSFLYSSSD 220
Db 194 LLDYLVQNTTISVNDTFQYIDISTFPLENVLSIFLYSNSD 234

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Job time: 86 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2001, 10:22:39 ; Search time 44.86 Seconds  
(without alignments)  
297.309 Million cell updates/sec

Title: US-09-628-126-19  
Perfect score: 1141  
Sequence: 1 MQVQGSVSPWRSTRPWS.....DTNFTPLDNLVSLFLYSSD 220

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1141	100.0	220	14 AAR45006	Sequence encoded b
2	1141	100.0	239	14 AAR45008	Sequence encoded b
3	814.5	71.4	215	14 AAR45007	Sequence encoded b
4	814.5	71.4	234	14 AAR45009	Sequence encoded b
5	742	65.0	143	21 AAB08277	Amino acid sequenc
6	600	52.6	143	21 AAB08276	Amino acid sequenc
7	112	9.8	279	17 AAR88357	Mouse Fas ligand.
8	109	9.6	179	16 AAR79069	Mouse Fas ligand (
9	109	9.6	279	16 AAR79098	Mouse Fas ligand.
10	104	9.1	279	16 AAR77282	Mouse Fas-L protei
11	97	8.5	138	16 AAR79068	Mouse Fas ligand (

12	97	8.5	143	21	AAB08266	Amino acid sequenc
13	95	8.3	137	16	AAR79067	Mouse Fas ligand (
14	92.5	8.1	258	20	AAV04371	Human Fas ligand d
15	91	8.0	179	16	AAR79066	Rat Fas ligand (pa
16	91	8.0	278	16	AAR79095	Rat Fas ligand enc
17	91	8.0	278	20	AAW98069	Rat Fas ligand (Fa
18	91	8.0	278	20	AAW95040	Rat FasL protein.
19	89	7.8	271	20	AAV28596	Fas ligand (FasL)
20	88.5	7.8	309	16	AAR64189	Murine 4-1BB-L pol
21	88.5	7.8	309	18	AAW26656	Murine 4-1BB ligan
22	88.5	7.8	448	21	AAB28694	FC-muAGP-1 (99-291
23	87	7.6	2013	21	AAB18265	Plasmodium falcipa
24	86.5	7.6	268	19	AAW18265	Non-cleavable Fas
25	86	7.5	319	22	AAB87774	Human TR44 amino
26	85	7.4	143	21	AAB08267	Amino acid sequenc
27	85	7.4	281	20	AAV04373	Human Fas ligand d
28	85	7.4	281	21	AAV87576	Human Fas ligand (
29	85	7.4	281	21	AAV87581	Human Fas ligand (
30	85	7.4	291	18	AAW19788	Mouse apoptosis in
31	85	7.4	291	19	AAW36762	Murine TRAIL polyp
32	85	7.4	291	19	AAW44353	Murine AGP-1. Mus
33	85	7.4	426	21	AAW28695	FC-muAGP-1 (120-29
34	84	7.4	265	19	AAW48954	Non-cleavable Fas
35	84	7.4	277	20	AAV04372	Human Fas ligand d
36	84	7.4	281	16	AAR77281	Human Fas-L protei
37	84	7.4	281	16	AAR79097	Human Fas ligand.
38	84	7.4	281	17	AAW98104	Human Fas ligand d
39	84	7.4	281	17	AAW88356	Human Fas ligand.
40	84	7.4	281	18	AAW27143	Human Fas ligand.
41	84	7.4	281	19	AAW75959	Human Fas ligand.
42	84	7.4	281	19	AAW49105	Fas ligand. Mamma
43	84	7.4	281	20	AAV28594	Wild type Fas liga
44	84	7.4	281	20	AAW98071	Human Fas ligand (
45	84	7.4	281	20	AAW95041	Human FasL protein

ALIGNMENTS

RESULT 1  
AAR45006  
ID AAR45006 standard; Protein; 220 AA.  
XX AAR45006;  
XX AC  
XX 19-JUN-1994 (first entry)  
XX Sequence encoded by a murine CD30-L cDNA clone.  
DE Hodgkin's disease; lymphoma; surface antigen; cytokine;  
KW CD30 ligand; CD30-L; TNF; NGF.  
XX Acomys cahirinus.  
XX Key Location/Qualifiers  
FH Region 28..48  
FT /label= transmembrane  
XX WO9324135-A.  
XX 09-DEC-1993.  
XX 25-MAY-1993; 93WO-US04926.  
XX 26-MAY-1992; 92US-0889717.  
PR 02-JUN-1992; 92US-0892459.  
PR 15-JUN-1992; 92US-0899660.  
PR 01-JUL-1992; 92US-0907224.  
PR 27-OCT-1992; 92US-0966775.  
XX (IMMV ) IMMUNEX CORP.  
XX Armitage RJ, Goodwin RG, Smith CA;

```

XX WPI; 1993-405417/50.
DR N-PSDB; AAQ53535.
XX
PT New cytokine, CD30-L, which binds CD30 - used for developing
PT prods. for diagnosis, detection, purifications, research and
PT therapy
XX
XX Claim 15; Figure 3a; 59pp; English.
XX
XX CD30-L is a ligand for CD30, the 120kd surface antigen widely used
XX as a clinical marker for Hodgkin's lymphoma and related haematologic
XX malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
XX L and other derived prods. can be used for elucidating the roles
XX that CD30 and CD30-L may play in the immune system and for diagnosis
XX and therapy. It can be isolated as follows. A cDNA library prepd. from
XX the murine helper T-cell line 7B9 is screened with a CD30/FC fusion
XX protein labelled with (125)I to obtain cDNA encoding murine CD30-L.
XX This cDNA can then be used as a probe to screen a human PBL cDNA
XX library to obtain cDNA encoding human CD30-L.
XX
XX Sequence 220 AA;
XX
XX Query Match 100.0%; Score 1141; DB 14; Length 220;
XX Best Local Similarity 100.0%; Pred. No. 2.2e-108;
XX Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MQVPGSVASPWRTSRPWRSTSRSYFYLTALVCLVAVAILLVVQKKDSTPNTTEK 60
Db 1 mqvpgsvaspwrtsrpwrstsrsyfytalvclvavaillvvqkdstpnttek 60
XX
QY 61 APLKGGNCSEDLFTCLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQ 120
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QY 121 FPGLYFIVCOLQFLVQCSNHSVDLTQLLINSKIKKOTLVTVCSGVQSKNIYQNLSQFL 180
Db 121 fpglyfivcolqflvqc snhsvdltql llnskikkotlv tvcesgvqskniyq nlsqfl 180
XX
QY 181 LHYLVQNSTISVRVDFNQYVDTNFPDLNLSVFLYSSSD 220
Db 181 lhylvqnstisvr vdnfqyvdtnfp dlnvlsvflysssd 220
XX
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ID AAR45008 standard; Protein; 239 AA.
XX
AC AAR45008;
XX
XX 19-JUN-1994 (first entry)
XX
DE Sequence encoded by a murine CD30-L cDNA clone
DE encoding additional N-terminal amino acids.
XX
XX Hodgkin's disease; lymphoma; surface antigen; cytokine;
XX CD30 ligand; CD30-L; TNF; NGF.
XX
XX Acomys cahirinus.
XX
XX Key Location/Qualifiers
XX FT Region 47..67
XX FT /label= Transmembrane
XX
PN W09324135-A.
XX
XX 09-DEC-1993.
XX
XX 25-MAY-1993; 93WO-US04926.
XX
XX 26-MAY-1992; 92US-0889717.
XX 02-JUN-1992; 92US-0892459.

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PR 15-JUN-1992; 92US-0899660.
PR 01-JUL-1992; 92US-0907224.
PR 27-OCT-1992; 92US-0966775.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Armitage RJ, Goodwin RG, Smith CA;
XX
XX WPI; 1993-405417/50.
XX N-PSDB; AAQ53537.
XX
XX New cytokine, CD30-L, which binds CD30 - used for developing
XX prods. for diagnosis, detection, purifications, research and
XX therapy
XX
XX Claim 15; Figure 6a; 59pp; English.
XX
XX CD30-L is a ligand for CD30, the 120kd surface antigen widely used
XX as a clinical marker for Hodgkin's lymphoma and related haematologic
XX malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
XX L and other derived prods. can be used for elucidating the roles
XX that CD30 and CD30-L may play in the immune system and for diagnosis
XX and therapy. It can be isolated as follows. A cDNA library prepd. from
XX the murine helper T-cell line 7B9 is screened with a CD30/FC fusion
XX protein labelled with (125)I to obtain cDNA encoding murine CD30-L
XX (AAQ53535). This cDNA can then be used as a probe to screen a human PBL
XX cDNA library to obtain cDNA encoding human CD30-L (AAQ53536). An
XX anchored PCR technique was employed to isolate CD30-L human and murine
XX clones containing an additional 19 N-terminal amino acid sequence
XX (AAQ53537, AAQ53538).
XX
XX Sequence 239 AA;
XX
XX Query Match 100.0%; Score 1141; DB 14; Length 239;
XX Best Local Similarity 100.0%; Pred. No. 2.4e-108;
XX Matches 220; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 MQVPGSVASPWRTSRPWRSTSRSYFYLTALVCLVAVAILLVVQKKDSTPNTTEK 60
Db 20 mqvpgsvaspwrtsrpwrstsrsyfytalvclvavaillvvqkdstpnttek 79
XX
QY 61 APLKGGNCSEDLFTCLKSTPSKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIQ 120
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Db 140 fpglyfivcolqflvqc snhsvdltql llnskikkotlv tvcesgvqskniyq nlsqfl 199
XX
QY 181 LHYLVQNSTISVRVDFNQYVDTNFPDLNLSVFLYSSSD 220
Db 200 lhylvqnstisvr vdnfqyvdtnfp dlnvlsvflysssd 239
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ID AAR45007 standard; Protein; 215 AA.
XX
XX AAR45007;
XX
XX 19-JUN-1994 (first entry)
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XX Sequence encoded by a human CD30-L cDNA clone.
XX
XX Hodgkin's disease; lymphoma; surface antigen; cytokine;
XX CD30 ligand; CD30-L; TNF; NGF.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX FT Region 22..43
XX FT /label= transmembrane

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[illegible]

ID AAB08277 standard; Protein; 143 AA.  
 AC AAB08277;  
 XX  
 DT  
 DE 04-DEC-2000 (first entry)  
 XX  
 DE Amino acid sequence of a mouse TNF ligand CD30L.  
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 KW AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;  
 KW type II transmembrane protein; B cell stimulatory factor;  
 KW inflammatory disorder; immune disorder; rheumatoid arthritis;  
 KW lupus and graft versus host disease.  
 XX  
 OS Mus sp.  
 XX  
 PN WO200047740-A2.  
 XX  
 PD 17-AUG-2000.  
 XX  
 PF 11-FEB-2000; 2000WO-US03653.  
 XX  
 PR 12-FEB-1999; 99US-0119906.  
 XX  
 PR 18-NOV-1999; 99US-0166271.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Boyle WJ, Hsu H;  
 XX  
 DR WPI; 2000-558217/51.  
 XX  
 PT Novel polypeptides comprising tumour necrosis factor ligand family  
 PT proteins, useful for treating inflammatory and immune disorders, e.g.  
 PT rheumatoid arthritis -  
 XX  
 PS Claim 14; Fig 9; 71pp; English.  
 XX  
 CC AAB08265-83 represent tumour necrosis factor (TNF) ligands. The  
 CC specification describes an AGP-3 polypeptide, which is TNF ligand  
 CC family member. AGP-3 is a type II transmembrane protein, and is a  
 CC potent B cell stimulatory factor. Expression of AGP-3 correlates to  
 CC increases in the number of B cells and immunoglobulins produced.  
 CC AGP-3 proteins, antibodies, and nucleic acids may be used to treat  
 CC inflammatory and immune disorders, e.g. rheumatoid arthritis,  
 CC Crohn's disease, lupus and graft versus host disease. The nucleic  
 CC acids may be used to regulate the expression of an AGP-3 related  
 CC protein. The AGP-3 proteins, antibodies and nucleic acids are also  
 CC useful for the detection of AGP-3 agonists, antagonists and  
 CC characterizing interactions with AGP-3 related proteins.  
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 SQ Sequence 143 AA;  
  
 Query Match 65.0%; Score 742; DB 21; Length 143;  
 Best Local Similarity 100.0%; Pred. No. 5.5e-68;  
 Matches 143; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 78 STPSKSWAYLQVSKHLNNTKLSWNEGTIHGLIYQDGNLIVQFPGLYFTVCOLQFLVQC 137  
 Db 1 stpskswaylqvskhlntkswnedgtihgliyqdgngliygqngliqfylvqlqlvqc 60  
  
 Qy 138 SNHSVDLTQLLLNSKIKKQTLVTVCESGVQSKNIYQNLISQFLHLHYLVQNSTISVRVDFN 197  
 Db 61 snhsvdltqlllnskkikktlvtvcsgvqskniyqnglsqfllhylvqnvstisvrvdnf 120  
  
 Qy 198 QYVDNTFPLDNVLSVFLYSSSD 220  
 Db 121 qyvdtntfpldnvlsvflysssd 143  
  
 RESULT 6  
 AAB08276  
 ID AAB08276 standard; Protein; 143 AA.  
 XX

AC AAB08276;  
 XX  
 DT 04-DEC-2000 (first entry)  
 XX  
 DE Amino acid sequence of a human TNF ligand CD30L.  
 XX  
 KW AGP-3; tumour necrosis factor ligand; TNF ligand; Crohn's disease;  
 KW type II transmembrane protein; B cell stimulatory factor;  
 KW inflammatory disorder; immune disorder; rheumatoid arthritis;  
 KW lupus and graft versus host disease.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200047740-A2.  
 XX  
 PD 17-AUG-2000.  
 XX  
 PF 11-FEB-2000; 2000WO-US03653.  
 XX  
 PR 12-FEB-1999; 99US-0119906.  
 XX  
 PR 18-NOV-1999; 99US-0166271.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Boyle WJ, Hsu H;  
 XX  
 DR WPI; 2000-558217/51.  
 XX  
 PT Novel polypeptides comprising tumour necrosis factor ligand family  
 PT proteins, useful for treating inflammatory and immune disorders, e.g.  
 PT rheumatoid arthritis -  
 XX  
 PS Claim 14; Fig 9; 71pp; English.  
 XX  
 CC AAB08265-83 represent tumour necrosis factor (TNF) ligands. The  
 CC specification describes an AGP-3 polypeptide, which is TNF ligand  
 CC family member. AGP-3 is a type II transmembrane protein, and is a  
 CC potent B cell stimulatory factor. Expression of AGP-3 correlates to  
 CC increases in the number of B cells and immunoglobulins produced.  
 CC AGP-3 proteins, antibodies, and nucleic acids may be used to treat  
 CC inflammatory and immune disorders, e.g. rheumatoid arthritis,  
 CC Crohn's disease, lupus and graft versus host disease. The nucleic  
 CC acids may be used to regulate the expression of an AGP-3 related  
 CC protein. The AGP-3 proteins, antibodies and nucleic acids are also  
 CC useful for the detection of AGP-3 agonists, antagonists and  
 CC characterizing interactions with AGP-3 related proteins.  
 XX  
 SQ Sequence 143 AA;  
  
 Query Match 52.6%; Score 600; DB 21; Length 143;  
 Best Local Similarity 77.3%; Pred. No. 1.6e-53;  
 Matches 109; Conservative 19; Mismatches 13; Indels 0; Gaps 0;  
  
 Qy 80 PSKSKSWAYLQVSKHLNNTKLSWNEGTIHGLIYQDGNLIVQFPGLYFTVCOLQFLVQCSN 139  
 Db 3 pfkkswaylqvskhlntkswnkdglhvryqdgngliygqngliqfylvqlqlvqc 62  
  
 Qy 140 HSDVLTQLLLNSKIKKQTLVTVCESGVQSKNIYQNLISQFLHLHYLVQNSTISVRVDFN 199  
 Db 63 nsdvlkllllnshkikktlvtvcsgmqtghvqnglsqfllhylvqnmstisvrndf 122  
  
 Qy 200 VDTNTPFLDNVLSVFLYSSSD 220  
 Db 123 idtstfpldnvlsflysssd 143  
  
 RESULT 7  
 AAB88357  
 ID AAB88357 standard; Protein; 279 AA.  
 XX  
 AC AAB88357;  
 XX

XX	Mus musculus.
OS	
XX	
PX	WO9513293-A1.
XX	
PD	18-MAY-1995.
XX	
PF	10-NOV-1994; 94WO-JP01899.
XX	
PR	18-OCT-1994; 94JP-0278378.
PR	10-NOV-1993; 93JP-0305975.
PR	13-DEC-1993; 93JP-0342526.
PR	18-MAR-1994; 94JP-0074344.
PR	08-JUL-1994; 94JP-0180955.
PR	07-SEP-1994; 94JP-0239363.
XX	
PA	(MOCH ) MOCHIDA PHARM CO LTD.
FA	(OSAB-) OSAKA BIOSCIENCE INST.
PI	Nagata S, Nakamura N, Suda T, Takahashi T;
XX	
DR	WPI: 1995-194031/25.
DR	N-PSDB: AAQ99498.
XX	
PT	Peptide which binds to Fas antigen, and antibody reactive with it -
PT	for treatment and diagnosis of viral or auto-immune diseases
XX	
PS	Claim 11; Page 222-224; 300pp; Japanese.
XX	
CC	Fas ligands or active fragments able to induce apoptosis in cells
CC	which express the Fas cell surface antigen are claimed. The
CC	proteins are isolated from human, rat and mouse sources. The present
CC	sequence represents part of the mouse Fas ligand.
XX	
SQ	Sequence 179 AA;
Query Match                  9.6%; Score 109; DB 16; Length 179;	
Best Local Similarity        26.2%; Pred. No. 0.0024:	
Matches     37; Conservative    28; Mismatches    46; Indels    30; Gaps	
OY	78 STPSKK-----SWAYLQSVKSHLNNTKLWNED-GT--IHGLIYQGDNLIVPFGLYFIVCQ 133       :     :     :     :     :     :     :     :     :
Ds	33 stpskkekprsvahitgnphrsiplewedygtalisgvykkkgglvinetglyfvysk 92     :     :     :     :     :     :     :     :     :
Oy	131 LOFLVQ-CSNHSVDLTQLLLNSK-----TKQTSLVTVCESG-----VQ 163 :       : : :       : : : : : : :   :   :   : vyfgrgsccndqlnhkvymr-nskypedlvimeekrlntcttgaiwahssylgvafnlts 151
Dd	169 SKNIYNLSQFLHLHYLVQNST 189 : ::l::ll:l   :   :
Dd	152 adhlvynisqslinfeeskt 172 : : l i n s q s l i n f e e s k t
RESULT	9
AAR79098	
ID	AAR79098 standard; Protein; 279 AA.
XX	
AC	AAR79098;
XX	
DT	21-FEB-1996 (first entry)
XX	
DE	Mouse Fas ligand.
XX	
KW	Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;
KW	Fas cell surface antigen; Fas-L; mouse.
OS	
MS	Mus musculus.
XX	
FH	Key Location/Qualifiers
FT	Region 25..78
FT	/label= proline-rich
FT	Domain 79..100









```

PR 08-JUL-1994; 94JP-0180955.
PR 07-SEP-1994; 94JP-0239363.
XX
XX (MOCH ) MOCHIDA PHARM CO LTD.
PA (OSAB-) OSAKA BIOSCIENCE INST.
XX
XX Nagata S, Nakamura N, Suda T, Takahashi T;
XX
XX WPI; 1995-194031/25.
DR N-PSDB; AAO99495.
XX
XX Peptide which binds to Fas antigen, and antibody reactive with it
PT for treatment and diagnosis of viral or auto-immune diseases
XX
XX Claim 7; Page 215-216; 300pp; Japanese.
XX
XX Fas ligands or active fragments able to induce apoptosis in cells
CC which express the Fas cell surface antigen are claimed. The
CC proteins are isolated from human, rat and mouse sources. The present
CC sequence represents part of the rat Fas ligand.
XX
XX Sequence 179 AA;
SQ

Query Match 8.0%; Score 91; DB 16; Length 179;
Best Local Similarity 24.2%; Pred. No. 0.16; Indels 40; Gaps 7;
Matches 37; Conservative 24; Mismatches 52;

Qy 78 SPPSK----KSWAYLQVSKHLNNTKLSWNEG-GT--IHGLIYQDGNLIVQPGLYFIVCQ 130
    ||||:  :| |:  :  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :
Db 33 stpsetkprsvahitgnprsrspilewedtygtalisgvykkgglvineaglyfvysk 92
    :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :
Qy 131 LQFLVQCSN-----HSV-----DLTLQLLINSKIKKQTLVTVCESGVQSKNIYQNL 176
    :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :
Db 93 vyfrrgscnsqplshkvymrnfkypgdvlvm-----eekklnycttg----- 134
    :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :
Qy 177 SQFLHLYQVNSTISVRVDNFQYVDNTEPLDN 209
    | |  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :
Db 135 -qlwahssylgavfnltvadhlvynisqisln 166
    :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :| |:  :

```

Search completed: September 5, 2001, 10:22:39  
Job time: 54 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2001, 10:29:28 ; Search time 50.89 seconds  
(without alignments)  
558.962 Million cell updates/sec

Title: US-09-628-126-23  
Perfect score: 1118  
Sequence: 1 MHVPAGSVASHLGTTSRSYF.....DTSTFPLENLVSLFLYSNSD 215

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_16.\*

- 1: sp-archaea.\*
- 2: sp-bacteria.\*
- 3: sp-fungi.\*
- 4: sp-human.\*
- 5: sp-invertebrate.\*
- 6: sp-mammal.\*
- 7: sp-mhc.\*
- 8: sp-organelle.\*
- 9: sp-phage.\*
- 10: sp-plant.\*
- 11: sp-rodent.\*
- 12: sp-unclassified.\*
- 13: sp-vertebrate.\*
- 14: sp-virus.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1094	97.9	234	043404	043404 homo sapien
2	100	8.9	169	11 Q9WV90	Q9WV90 marmota mon
3	94.5	8.5	234	6 Q9TTJ3	Q9TTJ3 equus caball
4	93.5	8.4	547	14 Q98269	Q98269 molluscum c
5	93	8.3	217	11 Q9ERG6	Q9ERG6 peromyscus
6	92	8.2	280	6 Q9MYL6	Q9MYL6 macaca neme
7	89.5	8.0	896	10 Q9M980	Q9M980 arabidopsis
8	88	7.9	1109	5 Q9GYH7	Q9GYH7 caenorhabdi
9	87.5	7.8	813	4 Q9V4N0	Q9V4N0 homo sapien
10	87.5	7.8	1003	4 Q9P207	Q9P207 homo sapien
11	85	7.6	761	3 Q9UVJ1	Q9UVJ1 candida alb
12	84.5	7.6	232	4 Q9UIV3	Q9UIV3 homo sapien
13	83.5	7.5	431	10 Q9LIF0	Q9LIF0 arabidopsis
14	83	7.4	372	14 Q96717	Q96717 chlorella v
15	83	7.4	636	2 Q56619	Q56619 vibrio chol
16	83	7.4	636	2 Q34235	Q34235 vibrio chol
17	83	7.4	636	2 Q87139	Q87139 vibrio chol
18	83	7.4	640	8 Q9GEV6	Q9GEV6 grammadenia
19	82.5	7.4	225	13 Q9IB42	Q9IB42 paralichthy

#### ALIGNMENTS

RESULT 1

O43404 ID O43404 PRELIMINARY; PRT; 234 AA.  
AC O43404;  
DT 01-JUN-1998 (TREMREL. 06, Created)  
DT 01-JUN-1998 (TREMREL. 06, Last sequence update)  
DE 01-MAR-2001 (TREMREL. 16, Last annotation update)  
DE CD30L PROTEIN.  
GN CD30L.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98007874; PubMed=9349718;  
RA Croager E.J., Abraham L.J.;  
RT "Characterisation of the human CD30 ligand gene structure.";  
RL Biochim. Biophys. Acta 1353:231-235(1997).  
DR EMBL; AF006384; AAB97877.1;  
DR EMBL; AF006381; AAB97877.1; JOINED.  
DR EMBL; AF006382; AAB97877.1; JOINED.  
DR EMBL; AF006383; AAB97877.1; JOINED.  
DR InterPro; IPR000478;  
DR InterPro; IPR003638;  
DR Pfam; PF00229; TNF; 1.  
DR ProDom; PD023087; 1.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PSS00049; TNF\_2; 1.  
DR SMART; SM00207; TNF; 1.  
SQ SEQUENCE 234 AA; 25963 MW; 37BA5733C7911751 CRC64;

Query Match 97.9%; Score 1094; DB 4; Length 234;  
Best Local Similarity 98.1%; Pred. No. 2.6e-101;  
Matches 211; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MHVPAGSVASHLGTTSRSYFYLTATLALCVFTVATIMLVVORTSIPNSPNVPLKG 60

DB 20 MHVPAGSVASHLGTTSRSYFYLTATLALCVFTVATIMLVVORTSIPNSPNVPLKG 79

QY 61 GNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSWNRKDLHLGVRYQDGNLVITQFPGLY 120

Db 80 GNCSEDLICLRAPFKKSWAYLQVAKHLNKTLSNWKDGLHGVRYQDGNLVQPPGLY 139  
Qy 121 FTICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTVCSGQTKHVVQNLQSLDLYLQ 180  
Db 140 FTICQLQFLVQCPNNSVDLKLLELLINKHKKQALVTVCSGQTKHVVQNLQSLDLYLQ 199  
Qy 181 VNTTISVNVDTFQYIDTSTFPLENVLISFLYSNSD 215  
Db 200 VNTTISVNVDTFQYIDTSTFPLENVLISFLYSNSD 234  
RESULT 2  
ID Q9WV90 PRELIMINARY; PRT; 169 AA.  
AC Q9WV90;  
DT 01-NOV-1999 (TrEMBLrel. 12, Created)  
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE FAS LIGAND (FRAGMENT).  
OS Marmota monax (Woodchuck).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciuridae; Sciurinae;  
OC Marmota.  
OX NCBI\_TaxID=9995;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=HEALTHY LIVER;  
RA Hodgson P.D., Grant M.D., Michalak T.I.;  
RT "Perforin and Fas/Fas ligand-mediated cytotoxicity in acute and  
chronic woodchuck viral hepatitis.",  
RL Clin. Exp. Immunol. 0:0-0(1999).  
DR EMBL; AF152368; AAD38387.1;  
DR InterPro: IPR000478;  
DR Pfam: PF00229; TNF\_1;  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
DR SMART; SM00207; TNF; 1.  
FT NON\_TER 1  
FT NON\_TER 169  
SQ SEQUENCE 169 AA; 19274 MW; FDE395B014717B6B CRC64;

Query Match 8.9%; Score 100; DB 11; Length 169;  
Best Local Similarity 24.6%; Pred. No. 0.024;  
Matches 32; Conservative 23; Mismatches 45; Indels 30; Gaps 5;  
Qy 71 LKRAPFKKSWAYLQVAKHLNKTLSNWKD---GILHGVRYQDGNLVQPPGLYFICQLQ 127  
Db 40 LRRA-----AHLTGKPNRSRSPLEWDTYGISLTSVGVYKQKGLVINDTGLYFVYSKIY 93  
Qy 128 FLVQ-CPNNSVDLKLLELLINKH-----IKQALVTVCSGM-----QTKH 166  
Db 94 FRGSCNNQPLSHKVVYKNSKYQDVLVMEGKMNYCTTGOMWARSYLGAVNFETNSDH 153  
Qy 167 VYQNLQSFLL 176  
Db 154 LYVNVSELSL 163

RESULT 3  
ID Q9TJ3 PRELIMINARY; PRT; 234 AA.  
AC Q9TJ3;  
DT 01-MAY-2000 (TrEMBLrel. 13, Created)  
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE TUMOR NECROSIS FACTOR-ALPHA.  
GN TNFA.  
OC Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;

RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=THORUGHRED; TISSUE=ARTERIAL ENDOTHELIUM;  
RA Ishida N., Sato F., Hasegawa T.;  
RT "Molecular cloning of equine tumor necrosis factor-alpha mRNA";  
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AB035735; BAA88349.1;  
DR HSSP; P01375; 4TSV.  
DR InterPro: IPR000478;  
DR Pfam: PF00229; TNF\_1;  
DR PRINTS; PR01234; TNECROSISFCT.  
DR PROSITE; PS00251; TNF\_1; 1.  
DR PROSITE; PS50049; TNF\_2; 1.  
DR SMART; SM00207; TNF; 1.  
SQ SEQUENCE 234 AA; 25430 MW; 2384D4950A21F377 CRC64;  
Query Match 8.5%; Score 94.5; DB 6; Length 234;  
Best Local Similarity 24.7%; Pred. No. 0.12;  
Matches 48; Conservative 33; Mismatches 88; Indels 25; Gaps 8;  
Qy 18 SYFLTATATLALCLVFTVATIMVLVWVTDSPNSPDVPLKGCNSEDLLCILKRAPFK 77  
Db 37 SFLLVAGATTFLCLLH----FGVIGPQREQLPNAFOSI-----NPLAQLRSSSRTPSD 87  
Qy 78 KSWAYLQVAKHLNKTLSW---NKDGIL-HGVRYQDGNLVQPPGLYFICQLQFLVQ-C 132  
Db 88 KPAHV-VANPOAEGQLWLSGRANALLANGVKLTDLQVPLDGLYLYISQVLFKGGC 146  
Qy 133 PNNSVDL--KLELLINKHKKQALVTVCSGMQT-----KHVQNLSOFLDLYQVN 182  
Db 147 PSTHVLTHTRISLAVSPSKVNLSSAISKLANTEPQAEAKPWEPYILGGVQLEKG 206  
Qy 183 TTISVNVDTFQYID 196  
Db 207 DQLSAEINQPNYLD 220

RESULT 4  
ID Q98269 PRELIMINARY; PRT; 547 AA.  
AC Q98269;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)  
DE MC102L.  
GN MC102L.  
OS Molluscum contagiosum virus subtype 1 (MCV1).  
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;  
OC Molluscipoxvirus.  
OX NCBI\_TaxID=10280;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96325459; PubMed=8670425;  
RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,  
RA Moss B.;  
RT "Genome sequence of a human tumorigenic poxvirus: prediction of  
specific host response-evasion genes";  
RL Science 273:813-816(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Senkevich T.G., Bugert J.J., Sisler J.R., Koonin E.V., Darai G.,  
RA Moss B.;  
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
DR EMBL; U60315; AAC55230.1;  
SQ SEQUENCE 547 AA; 60513 MW; 6A0C621DCF4B21AA CRC64;

Query Match 8.4%; Score 93.5; DB 14; Length 547;  
Best Local Similarity 24.8%; Pred. No. 0.41;  
Matches 51; Conservative 25; Mismatches 69; Indels 61; Gaps 12;  
Qy 3 VPAG-SVASH-----LGTTSRSYFLTT---ATLALCLVFTVATIMVLVQVQT-----DS 48

Query Match	8.3%;	Score 93;	DB 11;	Length 217;
Best Local Similarity	24.5%;	Pred. No. 0.16;		
Matches	49;	Conservative	31;	Mismatches 84; Indels 36; Gaps 9;
QY	18	SYFVLTTATLALCVETVATIMWLIVQVQRTSDIPNSPDNVPLKGGNCSEDLILCILKRAPFK	77	
Db	29	SFLIVAGATTIFCLL-----NFCVIGPQREEKFPN---NLPIGWSMAQTLTLRSSQNSSD	81	
QY	78	KSWAYLOVAKHLNKTKLW---NKKDGI-L-HGVRYODGNLVITQFPGLYFIICQLQFLVQ-C	132	
Db	82	KPAHV-VANHQVDEQLEWLSRRANALLANGMDLKNOLVIPADGLYLVYSQVLEKGGCC	140	
QY	133	PNN-----SVDLKLELILINKHKKQALVTVC-----ESGMOTKHVVYQNLSQFLL	176	
Db	141	SNYVLLHTTVSRFAVSIEDKVNLL-----SAIKSPCKETPEGSELKPWEIPIYLGCV	193	
QY	177	DYLOVNTTISVNDVTFQYID	196	
Db	194	FQLEKGDRLSAEVNLPKYLD	213	
RESULT	6			
Q9MYL6		PRELIMINARY;	PRT;	280 AA.
ID	Q9MYL6			
AC	Q9MYL6;			
DT	01-OCT-2000 (TremBLrel. 15, Created)			
DT	01-OCT-2000 (TremBLrel. 15, Last sequence update)			
DT	01-MAR-2001 (TremBLrel. 16, Last annotation update)			
DE	FAS LIGAND.			
GN	TR-FASL OR CM-FASL OR RM-FASL.			
OS	Macaca nemestrina (pig-tailed macaque),			

OS	Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey), and
OS	Macaca mulatta (Rhesus macaque).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC	Cercopitheciinae; Macaca.
OX	NCBI_TaxID=9545, 9541, 9544;
FN	[1]
RP	SEQUENCE FROM N.A.
RC	SPECIES=M.nemestrina; STRAIN=PIG-TAILED MONKEY;
RA	Kirii Y., Inoue T., Yoshino K.;
RT	"Pig-tailed monkey Fas ligand mRNA, complete cds.";
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
[2]	
RP	SEQUENCE FROM N.A.
RC	SPECIES=M.fascicularis; STRAIN=CYNOMOLGUS MONKEY;
RA	Kirii Y., Inoue T., Yoshino K.;
RT	"Cynomolgus monkey Fas ligand mRNA, complete cds.";
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
[3]	
RP	SEQUENCE FROM N.A.
RC	SPECIES=M.mulatta; STRAIN=RHESUS MONKEY;
RA	Kirii Y., Inoue T., Yoshino K.;
RT	"Rhesus monkey Fas ligand mRNA, complete cds.";
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR	EMBL; AB035140; BAA90296.1; -
DR	EMBL; AB035138; BAA90294.1; -
DR	EMBL; AB035139; BAA90295.1; -
DR	InterPro: IPR000478; -
DR	Pran; PF00229; TNF; 1.
DR	PRINTS; PR01234; TNECROSISFCF.
DR	PROSITE; PS00251; TNF_1; 1.
DR	PROSITE; PS00049; TNF_2; 1.
DR	SEQUENCE 280 AA; 31367 MW; F0B284D61A132EB4 CRC64;
Qy	75 PFKSW---AYLQVAKHLNKTLSWKD-GI--LHGVRVYDGNLVIOFGLYFIICLOF 128
Db	137 PEKKEQRKVAHLLTGKPNRSRSMPLWEDTYGIVLLSGYKKGGLVINETGLTFVPSKSV 196
Qy	129 LVQ-CPNNSVDLKLLELNKH-----IKKALVTCESGMQTKHVYQNLQSQFL----- 175
Db	197 RGQSTNLPLSHKYVMRNSKYPQDLYMGEKMSYCTTGQMAH-----SSYLGAVENTL 251
Qy	176 -LDYLQWNTTISVNVDTFFQIDTSTF 200
Db	252 SADHLNVNS---ELSLVNFEESQTF 274
RESULT	7
Q9M9B0	ID Q9M9B0 PRELIMINARY; PRT; 896 AA.
AC	Q9M9B0;
DT	01-OCT-2000 (TrEMBLrel. 15, Created)
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE	F27J15.13.
OC	Arabidopsis thaliana (Mouse-ear cress).
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC	Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC	Brassicales; Brassicaceae; Arabidopsis.
OX	NCBI_TaxID=3702;
FN	[1]
RP	SEQUENCE FROM N.A.
RA	Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
RA	Kim C., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L.,
RA	Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
RA	Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsy N., Nguyen M.,
RA	Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
RA	Toriiumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,

RA Ecker J.R.:  
RT "Genomic sequence for Arabidopsis thaliana BAC F27J15 from chromosome I.,"  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL: AC016041; AAF69701.1; -  
DR InterPro: IPR000719; -  
DR InterPro: IPR001245; -  
DR InterPro: IPR001611; -  
DR InterPro: IPR002290; -  
DR Pfam: PF00069; pkinase; 1.  
DR Pfam: PF00560; LRR; 3.  
DR PRINTS: PR00019; LEURICHRPT.  
DR PRINTS: PR00109; TYRKINASE.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS00011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
DR SMART: SM00220; S\_TKc; 1.  
KW ATP-binding; Serine/threonine-protein kinase; Transferase;  
KW Tyrosine-protein kinase.  
SQ SEQUENCE 896 AA; 99724 MW; A24500615125A15C CRC64;

Query Match 8.0%; Score 89.5; DB 10; Length 896;  
Best Local Similarity 22.1%; Pred. No. 1.8;  
Matches 45; Conservative 37; Mismatches 91; Indels 31; Gaps 9;

QY 4 PAGSVASHLGTSTRSYFYLTATLALCLVFTVIMVLVQRTDSIPNDVPLKGGNC 63  
DB 503 PCGNKPGEGCHPKKSIIVPVSSVALIALIALVFLVLRKNP-SRSKENG--RTSRS 559  
QY 64 SEDLLCILKRAPPKSWAYLOVAKHLNKTLSWKNKG---ILHGVRVODGNLVIQFPGLY 120  
DB 560 SEP-----PRITKKKFTVEVTMTNFRSVLKGFGVMVYHG--YVNGREQV----- 606  
QY 121 FTICQLQFLVQCPNNSVDLKLKLLINKHKK-QALVTVCSGQMOTKHVYO-----NLSQF 174  
DB 607 -AVKVLSHASKHGKHFKAEEVLLRVHKNLVSIVGCEKGKELALVYEMANGDLKEF 665  
QY 175 LL-----DYLVNTTISVNVDTFO 193  
DB 666 FSGKRGDDVLWRWETRLQIAVEAAQ 689

RESULT 8  
Q9GYH7 PRELIMINARY; PRT; 1109 AA.  
AC Q9GYH7;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE HYPOTHETICAL PROTEIN F49E7.1A.  
GN F49E7.1A.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
OC Rhabditidae; Pelodierinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RX MEDLINE=99069613; PubMed=9851916;  
RA None;  
RT "Genome sequence of the nematode C. elegans: a platform for  
investigating biology. The C. elegans Sequencing Consortium.,"  
RL Science 282:2012-2018(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RA Latreille P.;  
RT "The sequence of C. elegans cosmid F49E7.,"  
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;  
RA Waterston R.;  
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL: U64604; AAF98624.1; -  
SQ SEQUENCE 1109 AA; 125706 MW; 20BC3D321E6927DA CRC64;

Query Match 7.9%; Score 88; DB 5; Length 1109;  
Best Local Similarity 20.0%; Pred. No. 3.2;  
Matches 52; Conservative 37; Mismatches 83; Indels 88; Gaps 9;

QY 42 VVQRTDSIPNSPDNVPPLKGGNCSEDL-CILKRAPFKK-----SWAYLOVAKHLNKTCL 94  
DB 711 LIDGTASASTPRKEPLEPYSSENLVGCRAFQDTLRKMITVLGNISYLPRIGYRNKTKQ 770  
QY 95 S-WNKDGLHGVRYODGNLV-IQFPGLYFIICQLQFLVQC-----132  
DB 771 NEWDKVLLG--RFLDGVLVETEHRREYGLAAQLAEVRCEIPEFHAGVEILMDHLKLINE 828  
QY 133 -----PNNSVDLKLELLINKHKKQALV-----TVCSGQMOTKHV 167  
DB 829 AEQDKIVNGMREERASLMRKSNDISSLRQVLLNRLTEQILVDLFMTFLETGFNNKHT 888  
QY 168 -----YQNLQFLDYLVQVNTTISVNVDTFOYIDTS 198  
DB 889 VGKTQEVTAFLKFDYFKYLRADQERAEFLKLLTFLDRDLNQNVDMNFATDTMMSRAMT 948  
QY 199 TFPLENLSIF---LYSNSD 215  
DB 949 TIERYVIFAVYDNAFYPNRD 968

RESULT 9  
Q9Y4N0 PRELIMINARY; PRT; 813 AA.  
AC Q9Y4N0;  
DT 01-NOV-1999 (TREMBLrel. 12, Created)  
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE HYPOTHETICAL 90.6 KDA PROTEIN (FRAGMENT).  
GN DAFZP434C212.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=TESTIS;  
RA Ansoerge W., Wirkner U., Mewes H.W., Gassenhuber J., Wiemann S.;  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AL080196; CAB45770.1; -  
DR InterPro: IPR003123; -  
DR Pfam: PF02204; VPS9; 1.  
DR SMART: SM00167; VPS9; 1.  
KW Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 813 AA; 90632 MW; FB620567D606DD03 CRC64;

Query Match 7.8%; Score 87.5; DB 4; Length 813;  
Best Local Similarity 23.8%; Pred. No. 2.5;  
Matches 50; Conservative 28; Mismatches 65; Indels 67; Gaps 11;

QY 27 LALCLVTVATIMVLVYQRTDSIPNSPDNVPPLKGGNCSEDL-CILKRAPFKKSWAYLOVA 86  
DB 461 LALCSADSVAFPVLTHTSTHNGLPDHTDPE-----DNEIVCFKL-----VOIA 502  
QY 87 KHLNKTLSWKNKGILHGVRVODGNLVIQFPGLYFIICQLQFLVQCPNNSVDLKLLELIN 146  
DB 503 EAIN-----LQDKNLMAQLQETWRCVCRF-----DNRTCRKLLASIA 539  
QY 147 KHKKQ-----ALVTVCESGMOT--KHVYQNLQFLDYLVQVNTTISVNV-----188

```

RT the adenylate cyclase gene which complements CYR1 mutant as well as
RT six other genes including homologs of CHS6 and SAPI85.*;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ250310; CAB59913.1; -.
KW Hypothetical protein.
SQ SEQUENCE 761 AA; 87454 MW; 45B3AF011E57DD0E CRC64;

Query Match 7.6%; Score 85; DB 3; Length 761;
Best Local Similarity 24.7%; Pred. No. 4.2;
Matches 38; Conservative 26; Mismatches 50; Indels 40; Gaps

Qy 65 EDLLCILKRAPFKKSWAYLOVAKHLN--KTKLSNKNKGIL-----HGVRVQDGNLVIQFP 177
Db 551 EDLRTLTM-----ITIANNSNGERGALEWEMTGLIGWSVKHMLRDISLSLVTSSII 599

Qy 118 GL-----YFIICQL-----QFLVQCPNNRSVDILKELLINKHKIKKQALVTVCESGMQTK 165
Db 600 GKNVQGEFDYESTVOLLEIYDEFILDCPGYMDNYNGAFFSNKLTILRVSSKKMKDCS----- 654

Qy 166 HYYQNLSQ--FLDDY--LQVNTTISVNVDDTFQYI 195
Db 655 -LVKSLQGEYKFLDFVLLAIKILISWNVRWYQYV 687

RESULT 12
Q9UIV3 PRELIMINARY; PRT; 232 AA.
AC Q9UIV3;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE TUMOR NECROSIS FACTOR.

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OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93272029; PubMed=8499947;
RA Iris F., Bouqueleret L., Prieur S., Caterina D., Prinas G., Perrot V.,
RA Jurka J., Rodriguez-Tome P., Claverie J., Cohen D., Dausset J.;
RT "Dense Alu clustering and a potential new member of the NF kappa B
RT family within a 90 kilobase HLA class III segment.";
RL Nat. Genet. 3:137-145(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96215741; PubMed=8629302;
RA Utans U., Quist W.C., McManus B.M., Wilson J.E., Arceci R.J.,
RA Wallace A.F., Russell M.E.;
RT "Allograft inflammatory factory-1. A cytokine-responsive macrophage
RT molecule expressed in transplanted human hearts.";
RL Transplantation 61:1387-1392(1996).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=96008565; PubMed=7590964;
RA Holzinger I., de Baey A., Messer H.,
RA Weiss E.H.;
RT "Cloning and genomic characterization of LST1: a new gene in the human
RT TNF region.";
RL Immunogenetics 42:315-322(1995).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=93208881; PubMed=7916655;
RA Browning J.L., Ngam-ek A., Lawton P., Demarinis J., Tizard R.,
RA Chow E.P., Hession C., O'Brine-Greco B., Foley S.F., Ware C.F.;
RT "Lymphotoxin beta, a novel member of the TNF family that forms a
RT heteromeric complex with lymphotoxin on the cell surface.";
RL Cell 72:847-856(1993).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=86015093; PubMed=2995927;

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RESULT 14
Q96717          PRELIMINARY;      PRT;      372 AA.
ID Q96717;
AC Q96717;
DT 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)
DE DNA ADENINE METHYLTRANSFERASE.
GN M.CVISI.
OS Chlorella virus SC-1A.
OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phycodnavirus.
OX NCBI_TaxID=51374;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97341065; PubMed=9197539;
RA Qie Q., Zhang Y., Nelson M., Ropp S., Burbank D.E., Etten J.L.;
RT "Chlorella virus SC-1A encodes at least five functional and one
RT nonfunctional DNA methyltransferases.";
RL Gene 190:237-244(1997).
DR EMBL; U65736; AAC57943.1; -.
DR HSSP; P14385; IAQJ.
DR REBASE; 3013; M.Cvisi.
DR InterPro; IPR000051; -.
DR InterPro; IPR002052; -.
DR InterPro; IPR002296; -.
DR PRINTS; PR00507; N12N6WTFRASE.
DR PROSITE; PS00092; N6_MTASE; UNKNOWN_1.
KW transferase; Methyltransferase.
SQ SEQUENCE 372 AA; 42504 MW; A0F3B94287A2D0D2 CRC64;

Query Match          7.4%; Score 83; DB 14; Length 372;
Best Local Similarity 22.4%; Pred. No. 2.9;
Matches 33; Conservative 29; Mismatches 67; Indels 18; Gaps 5;

QY 32 VFTVATIMVLVQRTDSIPNSDPNP--LKGGNCSEDLILKRAPPKSWAVL--QVAK 87
DB 236 VEVKYGMMTKTLQ--DYFRNPEHIFVLKKDLCNKEI-----RFDKRLFDIKQIKT 286

QY 88 HLNKTLSWKNKGILHGVRQDGNLVIQFPGLFYICQLQFLVQCNPNSVDLKLELLINK 147
DB 287 HSGKCILMLRSNGVVMGSEYILRFSESESFLEDFICLVGIFGPDIDKVDLSLDIITSQ 346

QY 148 HIKQALVTVCESGMOTKHVYQNLSOF 174
DB 347 YLQK-----VCGSGRLTKNIMNLPF 368

RESULT 15
Q56619          PRELIMINARY;      PRT;      636 AA.
ID Q56619;
AC Q56619;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TReMBLrel. 15, Last annotation update)
DE O139 ORF1.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A11837;
RX MEDLINE=96417860; PubMed=8820651;
RA Comstock L.E., Michalski J.M., Johnson J.A., Morris J.G. Jr.,
RA Kaper J.B.;
RT "Cloning and sequence of a region encoding a surface polysaccharide of
RT Vibrio cholerae O139 and characterization of the insertion site in the
RT chromosome of Vibrio cholerae O1.";
RL Mol. Microbiol. 19:815-826(1996).
DR EMBL; U47057; AAC46243.1; -.
DR HSSP; P22106; ICT9.
DR InterPro; IPR00583; -.
DR InterPro; IPR001962; -.
```

```
DR Pfam; PF00310; GATase_2; 1.
DR Pfam; PF00733; Asn_synthase; 2. EE80FAE0EA8B1F36 CRC64;
SQ SEQUENCE 636 AA; 71948 MW; EE80FAE0EA8B1F36 CRC64;

Query Match          7.4%; Score 83; DB 2; Length 636;
Best Local Similarity 23.3%; Pred. No. 5.4;
Matches 40; Conservative 22; Mismatches 66; Indels 44; Gaps 5;

QY 58 LKGGNCSEDLILCIK-----RAPFKKSWAYLQVAKHLNKTLSWKNKGIL 102
DB 267 LSGGVDSSTVVGILQSLSTRPVKFTTIGFDHADFEASEASDVAKHLGTDHV----- 318

QY 103 HGVRYQDGNLVIQFPGLFYICQLQFLVQCNPNSVDLKLELLINKHIKKQALVTVCESGM 162
DB 319 -----ELIVSAEDALAIINQLPMVYDEPFADASQVPTFLVSKLAKKE--VTVCLSG- 367

QY 163 QTKHVIQNLSQFLLDYLVQNTTISVNVDTFOYIDTSTPLENVLSIFLYSNS 214
DB 368 -----DGGDELFCCYNRYHYTAKV----WSYLEKIPPIPKMLSVFLLTIS 409

Search completed: September 5, 2001, 10:29:30
Job time: 405 sec
```

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: September 5, 2001, 10:29:52 ; Search time 19.38 Seconds  
(without alignments)  
380.027 Million cell updates/sec

Title: US-09-628-126-23

Perfect score: 1118  
Sequence: 1 MHPVAGSVASHLGTTSRSYF.....DTSTFPLENLSIFLYNSND 215

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1118	100.0	234	1	TNF8_HUMAN
2	814.5	72.9	239	1	TNF8_MOUSE
3	112	10.0	279	1	FASL_MOUSE
4	96.5	8.6	234	1	TNFA_HORSE
5	94	8.4	233	1	TNFA_MACMU
6	94	8.4	235	1	TNFA_PERLE
7	92	8.2	233	1	TNFA_WACFA
8	90.5	8.1	281	1	FASL_HUMAN
9	90	8.1	233	1	TNFA_PAPHU
10	90	8.1	233	1	TNFA_PAPSP
11	89	8.0	809	1	YATA_SCHPO
12	86	7.7	278	1	FASL_RAT
13	85.5	7.6	309	1	41BL_MOUSE
14	85	7.6	233	1	TNFA_CANFA
15	85	7.6	235	1	TNFA_MOUSE
16	85	7.6	1220	1	CSAC_BACTU
17	84.5	7.6	232	1	TNFA_PIG
18	83.5	7.5	234	1	TNFA_SHEEP
19	83	7.4	1385	1	C5AA_BACUD
20	81.5	7.3	461	1	IP3K_HUMAN
21	81	7.2	233	1	TNFA_HUMAN
22	81	7.2	233	1	TNFA_WARMO
23	81	7.2	541	1	YHBX_ECOLI
24	81	7.2	1289	1	C5AB_BACUD
25	80.5	7.2	499	1	PPF5_RAT
26	80	7.2	229	1	TNFA_CEREL
27	80	7.2	235	1	TNFA_RAT
28	79.5	7.1	233	1	TNFA_BOVIN
29	79	7.1	800	1	PT11_YEAST
30	78.5	7.0	234	1	TNFA_CAVPO
31	78.5	7.0	426	1	MMML_YEAST
32	77.5	6.9	670	1	DD18_HUMAN
33	76	6.8	479	1	PAP1_VACCC

34	76	6.8	829	1	TOP1_XENLA
35	76	6.8	982	1	MSHM_SARGL
36	75.5	6.8	807	1	SUS1_ARATH
37	75	6.7	427	1	SYS_BUCAP
38	75	6.7	499	1	PPP5_HUMAN
39	74.5	6.7	745	1	RNR_BUCAI
40	74	6.6	851	1	RUD1_YEAST
41	74	6.6	2136	1	YCF2_MARPO
42	73.5	6.6	1178	1	PH81_YEAST
43	73	6.5	606	1	LEPA_BORBU
44	72.5	6.5	1900	1	STT4_YEAST
45	72	6.4	221	1	GP53_BPSP1

#### ALIGNMENTS

##### RESULT 1

ID	TNF8_HUMAN	STANDARD;	PRT;	234 AA.
AC	P32971;			
DT	01-OCT-1993 (Rel. 27, Created)			
DT	01-OCT-1993 (Rel. 27, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	CD30 LIGAND (CD30-L) (CD153 ANTIGEN).			
GN	TNFSF8 OR CD30LG OR CD30L.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93313964; PubMed=8391931;			
RA	Smith C.A., Gruess H.-J., Davis T., Anderson D., Farrah T.,			
RA	Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,			
RA	Grabstein K.H., Gliniak B., McAllister I.B., Fanslow W., Alderson M.,			
RA	Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.;			
RT	*CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose			
RT	ligand defines an emerging family of cytokines with homology to			
TNF.				
RL	Cell 73:1349-1360(1993).			
CC	-!- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF			
CC	T CELLS.			
CC	-!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.			
CC	-!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.			
CC	-!- DATABASE: NAME=PROW; NOTE=CD guide CD153 entry;			
CC	WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd153.htm"			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; L09753; AAA74594.1; -			
DR	PIR; A40710; A40710.			
DR	MIM; 603875; -			
DR	InterPro; IPR000478; -			
DR	Pfam; PF00229; TNF; 1.			
DR	PROSITE; PS00251; TNF_1; 1.			
DR	PROSITE; PS50049; TNF_2; 1.			
KW	Cytokine; Transmembrane; Glycoprotein; Signal-anchor.			
FT	DOMAIN 1 37			
FT	TRANSMEM 38 62			
FT	DOMAIN 63 234			
FT	CARBOHYD 81 81			
FT	CARBOHYD 109 109			
FT	CARBOHYD 153 153			
FT	CARBOHYD 189 189			
FT	CARBOHYD 201 201			
FT	CARBOHYD 234 234			
FT	SEQUENCE 234 AA; 26017 MW; C653615682305B1B CRC64;			

P41512	xenopus lae
O63852	sarcophyton
P49040	arabidopsis
P81434	buchnera ap
P53041	homo sapien
P57628	buchnera ap
P23236	saccharomyc
P09975	marichantia
P17442	saccharomyc
O51115	borrelia bu
P37297	saccharomyc
O48407	bacterioph

Query Match 100.0%; Score 1118; DB 1; Length 234;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-97;  
 Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSDPNPLKG 60  
 DB 20 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSDPNPLKG 79  
 QY 61 GNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVYODGNLVIQPPGLY 120  
 DB 80 GNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVYODGNLVIQPPGLY 139  
 QY 121 FTICQLQFLVQCPNNSVDLKLLELLINKHKIKQALVTVCSGQTKHVKYQNLQSLFDLYLQ 180  
 DB 140 FTICQLQFLVQCPNNSVDLKLLELLINKHKIKQALVTVCSGQTKHVKYQNLQSLFDLYLQ 199  
 QY 181 VNTTISVNVDTFQYIDTSTFPLENLSIFLYSNSD 215  
 DB 200 VNTTISVNVDTFQYIDTSTFPLENLSIFLYSNSD 234

RESULT 2

TNF8\_MOUSE  
 ID TNF8\_MOUSE STANDARD; PRT; 239 AA.  
 AC P32972;  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-OCT-1993 (Rel. 27, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE CD30 LIGAND (CD30-L).  
 GN TNFSF8 OR CD30LG OR CD30L.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID:10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-T-cell;  
 RX MEDLINE-93311364; PubMed-8391931;  
 RA Smith C.A., Gress H.-J., Davis T., Anderson D., Farrar T.,  
 RA Baker E., Sutherland G.R., Brannan C.I., Copeland N.G., Jenkins N.A.,  
 RA Grabstein K.H., Gliniak B., McAllister I.B., Fanslow W., Alderson M.,  
 RA Falk B., Gimpel S., Gillis S., Din W.S., Goodwin R.G., Armitage R.J.;  
 RT "CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose  
 RT ligand defines an emerging family of cytokines with homology to  
 RL Cell 73:1349-1360(1993).  
 CC -1- FUNCTION: BINDS TO THE CD30 RECEPTOR. INDUCES PROLIFERATION OF  
 CC T CELLS.  
 CC -1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC  
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 CC  
 CC EMBL: L09754; AAA74595.1; -;  
 DR PIR: B40710; B40710  
 DR MGD: MGI-88328; Tnfsf8.  
 DR InterPro: IPR000478; -;  
 DR Pfam: PF00229; TNF; 1.  
 DR PROSITE: PS00251; TNF\_1; 1.  
 DR PROSITE: PS00049; TNF\_2; 1.  
 KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.  
 FT DOMAIN 1 43 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 44 67 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
 FT DOMAIN 68 239 EXTRACELLULAR (POTENTIAL).  
 FT CARBOHYD 75 75 N-LINKED (GLCNAC. .) (POTENTIAL).

FT CARBOHYD 86 86 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 114 114 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 158 158 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 194 194 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 206 206 N-LINKED (GLCNAC. .) (POTENTIAL).  
 SQ SEQUENCE 239 AA; 26519 MW; 29003157DD425159 CRC64;  
 Query Match 72.9%; Score 814.5; DB 1; Length 239;  
 Best Local Similarity 70.6%; Pred. No. 5.1e-69;  
 Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;  
 QY 1 MHVPAGSVAS-----HLGTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPD 54  
 DB 20 MHVPAGSVASPMRSTRPWRSTRSRYFLSTAL-VCLVAVAILVLVQVKDSTPNTTE 78  
 QY 55 NVPLKGGNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVYODGNLVI 114  
 DB 79 KAPLKGNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSWKNKGILHGVYODGNLVI 138  
 QY 115 QPGLYFIICQLQFLVQCPNNSVDLKLLELLINKHKIKQALVTVCSGQTKHVKYQNLQSL 174  
 DB 139 QPGLYFIICQLQFLVQCPNNSVDLKLLELLINKHKIKQALVTVCSGQTKHVKYQNLQSL 198  
 QY 175 LLDYLVQNTTISVNVDTFQYIDTSTFPLENLSIFLYSNSD 215  
 DB 199 LLDYLVQNTTISVNVDTFQYIDTSTFPLENLSIFLYSNSD 239

RESULT 3

FASL\_MOUSE  
 ID FASL\_MOUSE STANDARD; PRT; 279 AA.  
 AC P41047; Q61217; Q9R1F2;  
 DT 01-FEB-1995 (Rel. 31, Created)  
 DT 01-FEB-1995 (Rel. 31, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE FAS ANTIGEN LIGAND.  
 GN TNFSF6 OR APTLIG1 OR FASL OR GLD.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID:10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM FASL).  
 RX MEDLINE-94185175; PubMed-7511063;  
 RA Takahashi T., Tanaka M., Brannan C.I., Jenkins N.A., Copeland N.G.,  
 RA Suda T., Nagata S.;  
 RT "Generalized lymphoproliferative disease in mice, caused by a point  
 RT mutation in the Fas ligand."  
 RL Cell 76:969-976(1994).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM FASL), AND 3D-STRUCTURE MODELING.  
 RC STRAIN=C57BL/6;  
 RX MEDLINE-95388076; PubMed-7544870;  
 RA Peitsch M.J., Tschoopp J.J.;  
 RT "Comparative molecular modelling of the Fas-ligand and other members  
 RT of the TNF family".  
 RL Mol. Immunol. 32:761-772(1995).  
 RN [3],  
 RP SEQUENCE FROM N.A. (ISOFORM FASL).  
 RX MEDLINE-95196085; PubMed-7889405;  
 RA Lynch D.H., Watson M.L., Alderson M.R., Baum P.R., Miller R.E.,  
 RA Tough T., Gibson M., Davis-Smith T., Smith C.A., Hunter K.;  
 RT "The mouse Fas-ligand gene is mutated in gld mice and is part of a  
 RT TNF family gene cluster."  
 RL Immunity 1:131-136(1994).  
 RN [4]  
 RP SEQUENCE FROM N.A. (ISOFORM FASL).  
 RC STRAIN=BALB/C;  
 RA Fenner M.H., Shioda T., Isselbacher K.J.;  
 RT "Mus musculus Balb/c Fas ligand differs from 129/SV Fas ligand in  
 RT two amino acids."  
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.

FN  
RP SEQUENCE FROM N.A. (ISOFORM FASLS).  
RC STRAIN=C3H; TISSUE=Spleen;  
RA MEDLINE=20021694; PubMed=10552956;  
RX Aylodi E., D'Adamo F., Zollo O., Agostini M., Moraca R.,  
RT Cannarile L., Migliorati G., Delfino D.V., Riccardi C.:  
"Cloning and expression of a short Fas ligand: A new alternatively  
spliced product of the mouse Fas ligand gene.";  
RL Blood 94:3456-3467(1999).  
[6]  
RN CHARACTERIZATION OF VARIANT GLD.  
RP MEDLINE=96091792; PubMed=7495745;  
RX Hahne M., Peitsch M.C., Imler M., Schroeter M., Lowin B.,  
RA Rousseau M., Bron C., Renno F., French L., Tschoop J.:  
"Characterization of the non-functional Fas ligand of gld mice.";  
RL Int. Immunol. 7:1381-1386(1995).  
CC -I- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT  
TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN  
CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.  
CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF  
PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE  
T CELLS, OR BOTH.  
CC -I- SUBUNIT: HOMOTRIMER (PROBABLE).  
CC -I- SUBCELLULAR LOCATION: ISOFORM FASL IS A TYPE II MEMBRANE PROTEIN.  
CC ISOFORM FASLS IS SOLUBLE.  
CC -I- ALTERNATIVE PRODUCTS: 2 ISOFORMS: FASL (SHOWN HERE) AND FASLS; ARE  
PRODUCED BY ALTERNATIVE SPLICING. ISOFORM FASL MEDIATES APOPTOSIS  
WHILE ISOFORM FASLS PREVENTS APOPTOSIS INDUCED BY FAS/FASL  
INTERACTION.  
CC -I- DISEASE: A DEFICIENCY IN THIS PROTEIN IS THE CAUSE OF GENERALIZED  
LYMPHOPROLIFERATION DISEASE (GLD), AN AUTOSOMAL RECESSIVE DISEASE  
RESPONSIBLE FOR LYMPHADENOPATHY AND AUTOANTIBODY PRODUCTION.  
CC -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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DR EMBL; U06948; AAA17800.1; -;  
DR EMBL; U10984; AAA19778.1; -;  
DR EMBL; S76752; AAB33780.1; -;  
DR EMBL; U58995; AAB02915.1; -;  
DR EMBL; AF119335; AAD52106.1; -;  
DR HSP; P01375; 2TUN.  
DR MGD; MGI:99255; Fasl.  
DR InterPro; IPR000478; -;  
DR Pfam; PF00229; TNF; 1.  
DR PROSITE; PS00251; TNF.1; 1.  
DR PROSITE; PS00049; TNF.2; 1.  
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis;  
KW Disease mutation; Alternative splicing.  
FT DOMAIN 1 78 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 79 100 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
FT DOMAIN 101 279 EXTRACELLULAR (POTENTIAL).  
FT DOMAIN 4 69 PRO-RICH.  
FT DOMAIN 45 51 POLY-PRO.  
FT DISULFID 200 231 BY SIMILARITY.  
FT CARBOHYD 117 117 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 258 258 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT VARSPLIC 1 210 MISSING (IN ISOFORM FASLS).  
FT VARIANT 184 184 T -> A (IN STRAIN BALB/C).  
FT VARIANT 218 218 E -> G (IN STRAIN BALB/C).  
FT VARIANT 273 273 F -> L (IN GLD; ABOLISHES BINDING OF FASL  
TO ITS RECEPTOR).  
SQ SEQUENCE 279 AA; 31442 MW; 37972E2728E0A1CA CRC64;

Query Match 10.0%; Score 112; DB 1; Length 279;  
Best Local Similarity 22.8%; Pred. No. 0.0024;  
Matches 38; Conservative 30; Mismatches 58; Indels 42; Gaps 6;  
QY 33 FTVATIMVLVVQRTDSIPNSPDVPLKGGNGCEDLLCLIKRAPFKKSWAYLQVAKHLNKT 92  
DB 115 FTQSLKVSFEKQIANPSTPSE-----KKEP--RSVAHLTGPHSRSI 156  
QY 93 KLSWNK---DGILHGVRQDNLVIOFPGLYFIICQQLVQ-CPNNSVDLKLLELLINKH 148  
DB 157 PLEWEDTYGTALISGVKYGKGLVINETGLYFVYSKVYFGQSCNNOPLNKHVYMRNSKY 216  
QY 149 -----IKQALVTVCESGM-----QTKHVVQNLSOFL 176  
DB 217 PEDLVLMEEKRLNYCTTGQIWAHSSYLGAVFNLTSADHLVYNISQLSL 264  
RESULT 4  
TNFA\_HORSE  
ID TNFA\_HORSE STANDARD; PRT; 234 AA.  
AC P29553;  
DT 01-APR-1993 (Rel. 25, Created)  
DT 01-APR-1993 (Rel. 25, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).  
GN TNF OR TNFA.  
OS Equus caballus (Horse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92084125; PubMed=1748301;  
RA Su X., Morris D.D., McGraw R.A.;  
RT "Cloning and characterization of gene TNF alpha encoding equine tumor  
necrosis factor alpha.";  
RL Gene 107:319-321(1991).  
CC -I- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE  
WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF  
CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF  
CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION  
OR BY STIMULATION OF INTERLEUKIN 1 SECRETION. IT CAN STIMULATE  
CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN  
CONDITIONS.  
CC -I- SUBUNIT: HOMOTRIMER.  
CC -I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
EXTRACELLULAR SOLUBLE FORM.  
CC -I- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY  
PROTEOLYTIC PROCESSING.  
CC -I- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
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DR EMBL; M64087; AAA30959.1; -;  
DR PIR; JQ1344; JQ1344.  
DR HSP; P01375; TNF.  
DR InterPro; IPR000478; -;  
DR InterPro; IPR002959; -;  
DR Pfam; PF00229; TNF; 1.  
DR PRINTS; PR01234; TNECROSISFCT.  
DR PRINTS; PR01235; TNFALPHA.  
DR PROSITE; PS00251; TNF.1; 1.  
DR PROSITE; PS00049; TNF.2; 1.  
KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.  
FT PROPEP 1 77 BY SIMILARITY.  
FT CHAIN 78 234 TUMOR NECROSIS FACTOR.  
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
FT

FT DISULFID 146 178 BY SIMILARITY.  
SQ SEQUENCE 234 AA; 25469 MW; E79ACE91143DF373 CRC64;

Query Match 8.6%; Score 96.5; DB 1; Length 234;  
Best Local Similarity 24.7%; Pred. No. 0.054; 88; Indels 25; Gaps 8;  
Matches 48; Conservative 33; Mismatches

Qy 18 SFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLKGGNCSEDLCLILKRAPFK 77

Db 37 SFLLVAGATTFLCLLH-----FGVIGPQREQLPNAFQSI-----NPLAOTLRSSSTPDS 87

Qy 78 KSWAYLQVAKHLNKTLSW---NKDGIL-HGVRYODGNLVIOFPGLYFIICQLQFLVQ-C 132

Db 88 KPAHV-VANPQAEQOLWLSGRANALLANGVKLTQNLVLPDLGLYLIYSQVLFKGGC 146

Qy 133 PNNSVDL---KLELLINKHKQALVTCESGMQT-----KHVYQNLISQFLLDYLOVN 192

Db 147 PSTHVLTLTISRLLAVSPSKVNLLSAISKSPCHTESPEQAQAKPWYPIYLGGVFQLEKG 206

Qy 183 TTISVNVDFQYID 196

Db 207 DLSAEINQPNYLD 220

Query Match 8.4%; Score 94; DB 1; Length 233;  
Best Local Similarity 25.2%; Pred. No. 0.092;  
Matches 51; Conservative 29; Mismatches 80; Indels 42; Gaps 11;

Qy 18 SYFYLTTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLKGGNCSEDLCLILKRAPF 76

Db 37 SFLLVAGATTFLCLLH-----FGVIGPQREQLPNAFQSI-----NPLAOTLRSSSTPDS 85

Qy 77 KSWAYLQVAKHLNKTLSW-NKDG---ILHGVRVYODGNLVIOFPGLYFIICQLQFLVQ- 131

Db 86 KPAHV-VANPQAEQOLWLSGRANALLANGVKLTQNLVLPDLGLYLIYSQVLFKGGC 144

Qy 132 CPNNSVDL-----KLELLINKHKQALVTCE---SGMQTKHYVQNLISQF 174

Db 145 CPNSHVLLTHTISRLLAVSVYQTKVNL-----SAIKSPQRETPGAQAKPWYPIYLG 197

Qy 175 LLDYLOVNTTISVNVDFQYID 196

Db 198 GVPLEKGDRLSAEINLPDYLD 219

RESULT 6

TNFA\_PERLE STANDARD; PRT; 235 AA.

ID TNFA\_PERLE STANDARD; PRT; 235 AA.

AC P36939;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).

GN TNF OR TNFA.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Macaca.

OX NCBI\_TaxID=9544;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=96003435; PubMed=7561102;

RT Villing F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;

RT "Comparative sequence analysis of cytokine genes from human and

nonhuman primates.";

RL J. Immunol. 155:3946-3954(1995).

CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE

CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF

CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF

CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION

CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE

CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN

CC CONDITIONS.

CC -!- SUBUNIT: HOMOTRIMER.

CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN

CC EXTRACELLULAR SOLUBLE FORM.

CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY

CC PROTEOLYTIC PROCESSING.

CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING

CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH

CC AND MALNUTRITION.

CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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CC -----

DR EMBL; U19850; AAA86712.1;

DR HSSP; P01375; ITNF.

CONDITIONS.

-1- SUBUNIT: HOMOTRIMER.

-1- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM.

-1- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTEOLYTIC PROCESSING.

-1- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH AND MALNUTRITION.

-1- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.

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EMBL; AB000513; BAA19131.1; -

HSSP; P01375; 1TNE.

InterPro; IPR000478; -

InterPro; IPR002959; -

Pfam; PF00229; TNE; 1

PRINTS; PRO1234; TNECOSISFCT.

PRINTS; PRO1235; TNFALPHA.

PROSITE; PS00251; TNF\_1; 1.

PROSITE; PS50049; TNF\_2; 1.

Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.

PROPEP 1 76 BY SIMILARITY.

CHAIN 77 233 TUMOR NECROSIS FACTOR.

FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).

FT DISULFID 145 177 BY SIMILARITY.

SEQUENCE 233 AA; 25558 MW; 6ABF2C3AB132C217 CRC64;

-----

Query Match 8.2%; Score 92; DB 1; Length 233;

Best Local Similarity 24.4%; Pred. No. 0.14;

Matches 51; Conservative 32; Mismatches 82; Indels 44; Gaps 11;

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QY 16 SRSYFYLTATLALCLVFTVATIMVL-----VQRTDSIENSPDNV-PLKGCNSEDLLC 69  
|| : : : : || : : : : : : : : : : || : : : : ||

Db 27 SRRCWFL--SLFSFLLVAGAATFLCLLHFGVIGPQREFFKPSLSPLAQAVRSS--- 80  
|| : : : : || : : : : : : : : : : || : : : : ||

QY 70 ILKRAPKKSWAYLOVAKHLNKTKLSW-NKDG---ILHGVRYODGNLVIQPGLYFIQC 125  
|| : : : : || : : : : : : : : : : || : : : : ||

Db 81 --SRTSDKPAHV-VANPOAEGQLWNRNALVANGVELTDNLQLVPSSEGLYLIYSQ 137  
|| : : : : || : : : : : : : : : : || : : : : ||

QY 126 LQFLVQ-CPNNSVDL-----KLELLINKHIKQALVTVCE---SGMQTKHV 167  
|| : : : : || : : : : : : : : : : || : : : : ||

Db 138 VLFKGGCPCSNHVLTHTSIRAVSYQTKVNL-----SAIKSPQRETPEGAEPKW 190  
|| : : : : || : : : : : : : : : : || : : : : ||

QY 168 QNLSQELLDYLQVNTTISVNVDTFFQID 196  
|| : : : : || : : : : : : : : : : || : : : : ||

Db 191 YEPIYLGGVFQLEKGRDLSEINLPDYLD 219  
|| : : : : || : : : : : : : : : : || : : : : ||

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RESULT 8

FASL\_HUMAN

ID FASL\_HUMAN STANDARD; PRT; 281 AA.

AC P48023;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 01-OCT-2000 (Rel. 40, Last annotation update)

DE FAS ANTIGEN LIGAND (APOPTOSIS ANTIGEN LIGAND) (APTL).

GN TNFSF6 OR APTLIG1 OR FASL.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OC NCBI\_Taxid=9606;

RN [1]

RX MEDLINE=95105731; PubMed=7528780;

-----

RA Alderson M.;  
 RT "Fas ligand mediates activation-induced cell death in human T lymphocytes";  
 RL J. Exp. Med. 181:71-77(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95127360; PubMed=7826947;  
 RA Takahashi T., Tanaka M., Inazawa J., Abe T., Suda T., Nagata S.;  
 RT "Human Fas ligand: gene structure, chromosomal location and species specificity";  
 RL Int. Immunol. 6:1567-1574(1994).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Schaeuble C.E., Poehlmann R., Philippson P., Eibel H.;  
 RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95071350; PubMed=7980502;  
 RA Mita E., Hayashi N., Iio S., Takehara T., Hijioka T., Kasahara A.,  
 RA Fusamoto H., Kamada T.;  
 RT "Role of Fas ligand in apoptosis induced by hepatitis C virus infection";  
 RL Biochem. Biophys. Res. Commun. 204:468-474(1994).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Wilkinson J.;  
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.  
 RN [6]  
 RP SEQUENCE OF 1-10 FROM N.A.  
 RC TISSUE=Blood;  
 RA Matsumura M., Nakanishi Y., Ohba Y.;  
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.  
 CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE T CELLS, OR BOTH.  
 CC -!- SUBUNIT: HOMOTRIMER (PROBABLE).  
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FROM THE CELL SURFACE.  
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; X89102; CA61474.1; -;  
 DR EMBL; U08137; AAC50071.1; -;  
 DR EMBL; U11821; AAC50124.1; -;  
 DR EMBL; D38122; BAA07320.1; -;  
 DR EMBL; Z96050; CAB09424.1; -;  
 DR EMBL; AB013303; BAA32542.1; -;  
 DR HSPF; P01375; 2TUN.  
 DR MIN; 134638; -;  
 DR InterPro; IPR000478; -;  
 DR Pfam; PF00229; TNF; 1.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis.  
 FT DOMAIN 1 80  
 FT TRANSMEM 81 102  
 FT DOMAIN 103 281  
 FT DOMAIN 4 70  
 FT DOMAIN 45 65  
 FT DISULFID 202 233  
 FT CARBOHYD 184 184  
 FT CARBOHYD 250 250

FT CARBOHYD 260 260 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 281 AA; 31485 MW; A0A6EB358246E9BB CRC64;  
 Query Match 8.1%; Score 90.5; DB 1; Length 281;  
 Best Local Similarity 26.4%; Pred. No. 0.24;  
 Matches 34; Conservative 21; Mismatches 47; Indels 27; Gaps 6;  
 QY 75 PFKSW---AYLQVAKHLNKTLSWKNK-GI--LHGVRQDGNLVQFPGLYFIICQLQF 128  
 DB 138 PEKKELRKVAHLTKGKSNRSMPLWEDYIGVLLSVKYGKGLVNETGLYFYVSKYVF 197  
 QY 129 LVQ-CPNNSVDKLELLINKH-----IKKQALVTVCESGM-----QTKHV 167  
 DB 198 RQGCNNLPLSHKVMRNSKYPQDLVMMEGKMSYCTTGQMMARSSYLCAVFNLSADHL 257  
 QY 168 YQNLSQFLL 176  
 DB 258 YVNVSELSL 266  
 RESULT 9  
 TNFA\_PAPHU STANDARD; PRT; 233 AA.  
 AC 077510;  
 DT 15-DEC-1998 (Rel. 37, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).  
 GN TNF OR TNFA.  
 OS Papio hamadryas ursinus (Chacma baboon).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;  
 OC Cercopithecoidea; Papio.  
 OX NCBI\_TaxID=36229;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98147379; PubMed=9488055;  
 RA Haudek S.B., Redl H., Schlag G., Giroir B.P.;  
 RT "Complementary DNA (cDNA) sequence of baboon tumor necrosis factor alpha";  
 RL Mol. Immunol. 34:1041-1042(1997).  
 CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN CONDITIONS.  
 CC -!- SUBUNIT: HOMOTRIMER.  
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN EXTRACELLULAR SOLUBLE FORM.  
 CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY PROTEOLYTIC PROCESSING.  
 CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH AND MALNUTRITION.  
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; AF019963; AAC31675.1; -;  
 DR InterPro; IPR000478; -;  
 DR InterPro; IPR002959; -;  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR PRINTS; PR01235; TNFALPHA.



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DR HSP; P01375; 1TNF.
DR InterPro; IPR000478; -.
DR InterPro; IPR002959; -.
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRINTS; PR01235; TNFALPHA.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00251; TNF_2; 1.
DR Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;
KW Myristate.
FT PROPEP 1 76 BY SIMILARITY.
FT CHAIN 77 233 TUMOR NECROSIS FACTOR.
FT TRANSMEM 36 56 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT LIPID 19 19 MYRISTATE (BY SIMILARITY).
FT LIPID 20 20 MYRISTATE (BY SIMILARITY).
FT DISULFID 145 177 BY SIMILARITY.
FT SEQUENCE 233 AA; 25557 MW; 455360848DC74173 CRC64;

Query Match 8.1%; Score 90; DB 1; Length 233;
Best Local Similarity 24.8%; Pred. No. 0.22;
Matches 50; Conservative 30; Mismatches 80; Indels 42; Gaps 11;

QY 18 SYPLTATIALCLIVFTVATIMVLVQRTSDIPNSPDV-PLKGNGCSEDLCLTKRAPF 76
   | : | | | | : | | | : | | : | | | | | | | | | |
Db 37 SELLVAGATTFLCLH-----FGVIGPQR-EEFPKDPSLSLAQAVRSS-----SRTPS 85

QY 77 KSWAYLOVAKHLNKTLSW-NKDG---ILHGVRQDGNLVQIOPGLYFIICQLQFLVQ- 131
   | | | | | : | | | | : | | : | | | | | | | | | |
Db 86 DKPAHV-VANPQAEQQLWRANRANLALLANGVELRDNLVWPSEGUYLYISQVLFKGG 144

QY 132 CPNNSVDL-----KLELNKHKKQALVTGCE-----SGMQTKHVVQNLSQF 174
   | | | | | : | | | | : | | : | | | | | | | | | |
Db 145 CPSTHVLTLTISRIVSYQTKNLL-----SAIKSPQRETPEGAEPWEPYILG 197

QY 175 LDLYLQVNTTISVNDVTFQYID 196
   : | : | : | : | : | : | : | : | : | : | : | : |
Db 198 GVFOLEKGDRLSAEINLPDYID 219

RESULT 11
YATA_SCHPO
ID YATA_SCHPO STANDARD; PRT; 809 AA.
AC Q10155;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-JUL-1998 (Rel. 36, Last annotation update)
DT HYPOTHETICAL 90.6 KDA PROTEIN CID4.10 IN CHROMOSOME I.
GN SPAC1D4.10.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OC NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RC Lye G., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO S.POMBE SPBC3D5.03C AND SOME, TO YEAST YKR079C.
-----
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-----
CC EMBL; Z69239; CAA93219.1; -.
DR DR
DR HSP; P15039; 1PRV.
KW Hypothetical protein.
SQ SEQUENCE 809 AA; 90602 MW; 350PBE7B05PBF880 CRC64;

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Query Match      8.0%; Score 89; DB 1; Length 809;
Best Local Similarity 29.1%; Pred. No. 1.2;
Matches 30; Conservative 14; Mismatches 33; Indels 26; Gaps 5;

QY 117 PGLYFIICQLQFLVQCPNNSVDLKLELLNKHKKKQALVTVCSGQTKHYQN----- 170
    || | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 324 PGSSF-----PIIHCNP---ELVIDLVNIENHKWTNAPKPCVIVHSVTPEVKNPQSW 374
    || | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 171 LSQF-----LLDYLQVNTTI-----SVNVDYFOYDSTSTPL 202
    || | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 375 ISSFFSEVSHLIASTEVEVNIYPRSAVAIATLNLDSKVPEPL 417
    || | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 12
FASL_RAT
ID FASL_RAT STANDARD; PRT; 278 AA.
AC P36940;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE FAS ANTIGEN LIGAND.
GN TNFSF6 OR APILG1 OR FASL.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94084792; PubMed=7505205;
RA Suda T., Takahashi T., Golstein P., Nagata S.;
RT "Molecular cloning and expression of the Fas ligand, a novel member
RT of the tumor necrosis factor family.";
RL Cell 75:1169-1178(1993).
CC -!- FUNCTION: CYTOKINE THAT BINDS TO FAS ANTIGEN, A RECEPTOR THAT
CC TRANSDUCES THE APOPTOTIC SIGNAL INTO CELLS. MAY BE INVOLVED IN
CC CYTOTOXIC T CELL MEDIATED APOPTOSIS AND IN T CELL DEVELOPMENT.
CC FAS-ANTIGEN MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE INDUCTION OF
CC PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED SUICIDE OF MATURE
CC T CELLS, OR BOTH.
CC -!- SUBUNIT: HOMODIMER (PROBABLE).
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. MAY BE RELEASED
CC INTO THE EXTRACELLULAR FLUID, PROBABLY BY CLEAVAGE FORM THE CELL
CC SURFACE.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ACTIVATED SPLENOCYTES AND
CC THYMOCYTES. MODERATE OR WEAK EXPRESSION FOUND IN SMALL INTESTINES,
CC KIDNEY AND LUNG.
CC -!- INDUCTION: BY PMA/IONOMYCIN AND CONCAVALIN/INTERLEUKIN-2.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U03470; AAC52129.1; -
DR InterPro; IPR000478; -
DR Pfam; PF00229; TNF_1; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor; Apoptosis.
FT DOMAIN 1 77 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 78 99 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 100 278 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 4 69 PRO-RICH.
FT DOMAIN 45 58 POLY-PRO.
FT DISULFID 199 230 BY SIMILARITY.
FT CARBOHYD 116 116 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 247 247 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 278 AA; 31140 MW; 2898E18A62CEAC6 CRC64;

Query Match      7.7%; Score 86; DB 1; Length 278;
Best Local Similarity 23.6%; Pred. No. 0.63;
Matches 29; Conservative 21; Mismatches 49; Indels 24; Gaps 4;

QY 78 KSWAYLQVAKHLNKTLSWNK---DGILHGVRYQDGNLVIQFPGLYFIICQLQFLVQ-CP 133
    :| | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 141 RSVAHLTGNPSPRSIPLEWEDTYGTALISGVYKKGGLVINEAGLYFVYSKVYFRGOSCN 200
    :| | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
QY 134 NNSVDLKLELLNKH-----IKQALVTVCSGM-----QTKHYQNLSQ 173
    :| | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
DB 201 SQPLSHRVYMRNFYPGDLVLMEEKLNKYCTGQIWAHSSYLGAVFNLTVADHLYVNISQ 260
    :| | :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

QY 174 FLL 176
DB 261 LSL 263

RESULT 13
41BL_MOUSE
ID 41BL_MOUSE STANDARD; PRT; 309 AA.
AC P41274;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 4-1BB LIGAND (4-1BBL).
GN TNFSF9 OR LY63L OR CD137L OR CD157L.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RT TISSUE=T-cell;
RX MEDLINE=94009225; PubMed=8405064;
RA Goodwin R.G., Din W.S., Davis-Smith T., Anderson D.M., Gimpel S.D.,
RA Sato T.A., Maliszewski C.R., Brannan C.I., Copeland N.G., Smith C.A.;
RA Jenkins N.A., Farrar T., Armitage R.J., Fanslow W.C., Smith C.A.;
RT "Molecular cloning of a ligand for the inducible T cell gene 4-1BB: a
RT member of an emerging family of cytokines with homology to tumor
RT necrosis factor.";
RL Eur. J. Immunol. 23:2631-2641(1993).
CC -!- FUNCTION: INDUCES THE PROLIFERATION OF ACTIVATED PERIPHERAL BLOOD
CC T CELLS. MAY HAVE A ROLE IN ACTIVATION-INDUCED CELL DEATH (AICD).
CC MAY PLAY A ROLE IN COGNATE INTERACTIONS BETWEEN T CELLS AND
CC B CELLS/MACROPHAGES.
CC -!- SUBUNIT: HOMODIMER (PROBABLE).
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; LJ5435; AAA39435.1; -
DR MGD; MGI:1101058; Tnfsf9.
DR InterPro; IPR000478; -
DR Pfam; PF00229; TNF_1; 1.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS50049; TNF_2; 1.
KW Cytokine; Transmembrane; Glycoprotein; Signal-anchor.
FT DOMAIN 1 82 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 83 103 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).
FT DOMAIN 104 309 EXTRACELLULAR (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).

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FT CARBOHYD 293 293 N-LINKED (GLCNAC.....) (POTENTIAL).
SQ SEQUENCE 309 AA; 33853 MW; 2A425829AD6B89C0 CRC64;

Query Match
Best Local Similarity 23.5%; Pred. No. 0.8; Length 309;
Matches 52; Conservative 38; Mismatches 78; Indels 53; Gaps 12;

QY 27 LALCLVFTVATIMLVVQRTDSTP-----NSPDNV-PLKGGNCSEDLCLCIL 71
DB 87 VALVLLLLIAA-CVPIFTREPRPALTTITSPNLGTRENNADQVTPVSHIGCPN---TTQ 142
QY 72 KRAP-FKKSWAYLVQAKHLNKLKLSW-NKDG-----ILHGVRYODG---NLVIQPPGLYFI 122
DB 143 QGSPVFAKLARKNOAS--LCNTTLNHSQDGAGSSYLSQGLRYEEDKKELVVDSPGLYYV 200
QY 123 IGOFLVQCPNN-----SVDLKLELLINKHKKQALVTVCESGMQTKHYVONLSQF 174
DB 201 FLEKLSPTFTTGHKVGQWSVLVLAQKQVDFEDNLALTVELFPSCNEKLVDRWSQL 260
QY 175 LLDYLVQNTTISVNVDTF-----QYIDTSTFPL 202
DB 261 LL--LKAGHRLSVGLRAYLHGAQDAYRDWELSYPTNTSFL 299

RESULT 14
TNFA_CANFA STANDARD; PRT; 233 AA.
AC P51742; Q28339;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN TNF OR TNFA.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RA Piers W., Beernaert M.;
RP SEQUENCE FROM N.A.
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RA Zuckerk K., Lu P., Fuller L., Asthana D., Esquenazi V., Miller J.;
RT "Cloning and expression of the cDNA for canine tumor necrosis
factor-alpha in E. coli.";
RL Lymphokine Res. 13:191-196(1994).
RN [3]
RP SEQUENCE OF 74-205 FROM N.A.
RC STRAIN-BEAGLE; TISSUE=Blood;
RA Gilmore W.H., Carter S.D., Bennett M., Barnes A., Kelly D.F.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE
CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF
CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF
CC CACHEXIA, IT IS A POTENT PROGEN CAUSING FEVER BY DIRECT ACTION
CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE
CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN
CC CONDITIONS.
CC -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN
CC EXTRACELLULAR SOLUBLE FORM (BY SIMILARITY).
CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY
CC PROTEOLYTIC PROCESSING (BY SIMILARITY).
CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING
CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH
CC AND MALNUTRITION.
CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.
CC -----
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CC -----
DR EMBL; X94932; CAA64403.1; -
DR EMBL; S74068; AAB32391.1; -
DR EMBL; Z70046; CAA93908.1; -
DR HSSP; P01375; 1TNF.
DR InterPro; IPR000478; -
DR InterPro; IPR002959; -
DR Pfam; PF00229; TNF; 1.
DR PRINTS; PR01234; TNECROSISFCT.
DR PRINTS; PR01235; TNFALPHA.
DR PROSITE; PS00251; TNF_1; 1.
DR PROSITE; PS00049; TNF_2; 1.
KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor.
FT PROPEP 1 76
FT CHAIN 77 233
FT TRANSMEM 36 56
FT DISULFID 145 177
FT CONFLICT 59 60
FT CONFLICT 66 66
FT CONFLICT 74 74
FT CONFLICT 111 111
FT CONFLICT 116 116
FT CONFLICT 134 135
SQ SEQUENCE 233 AA; 25447 MW; 7B2588FBC8B25340 CRC64;

Query Match 7.6%; Score 85; DB 1; Length 233;
Best Local Similarity 23.8%; Pred. No. 0.64;
Matches 49; Conservative 32; Mismatches 75; Indels 50; Gaps 11;

QY 18 SYFYLTATLALCLVFTVATIMLVVQRTDSTP-----SPDNVPLKGGNCSEDLCLILK 72
DB 37 SFLLVAGATTFTCLLH-----FGVIGPQR-EELPNGLQLISPLAQTVKSS----- 81
QY 73 RAPFKSWAYLVQAKHLNKLKLSW---NKDGIL-HGVRYQDGNLVQFPGLYFIICQLQF 128
DB 82 RTPSDKPVAVH-VANPEAGQLWLSRRANALLANGVELTDNLQIVPSDGLIYSQVLF 140
QY 129 LVQ-CPNNSVDL-----KLELLINKHKKQALVTVC-----SGMQTKHYVON 170
DB 141 KGQGPCSTHVLTLTISRFAVSQTKVNL-----SAIKSPCQRETPGTEARPWYEP 193
QY 171 LSQFLLDLYLVQNTTISVNVDTFQYID 196
DB 194 IYLGCVFQLEKGDRLSAEINLPNYLD 219

RESULT 15
TNFA_MOUSE STANDARD; PRT; 235 AA.
ID TNFA_MOUSE
AC P06804; Q62326;
DT 01-JAN-1988 (Rel. 05, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE TUMOR NECROSIS FACTOR PRECURSOR (TNF-ALPHA) (CACHECTIN).
GN TNF OR TNFA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Shirai T., Shimizu N., Shiojiri S., Horiguchi S., Ito H.;
RT "Cloning and expression in Escherichia coli of the gene for mouse
tumor necrosis factor.";
RL DNA 7:193-201(1988).
RN [2]
RP SEQUENCE FROM N.A.
```

RX MEDLINE=85298296; PubMed=3898078;  
 RA Pennica D., Hayflick J.S., Bringham T.S., Palladino M.A.,  
 RA Goeddel D.V.;  
 RT "Cloning and expression in *Escherichia coli* of the cDNA for murine  
 RT tumor necrosis factor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:6060-6064(1985).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=86149365; PubMed=2419912;  
 RA Caput D., Beutler B., Hartog K., Thayer R., Brown-Shimer S.,  
 RA Cerami A.;  
 RT "Identification of a common nucleotide sequence in the  
 RT 3'-untranslated region of mRNA molecules specifying inflammatory  
 RT mediators.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:1670-1674(1986).  
 RN [4]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=85242112; PubMed=2989794;  
 RA Fransen L., Mueller R., Marmenout A., Tavernier J., van der Heyden J.,  
 RA Kawashima E., Chollet A., Tizard R., van Heuverswyn H., van Vliet A.,  
 RA Ruysschaert M.-R., Fiers W.;  
 RT "Molecular cloning of mouse tumour necrosis factor cDNA and its  
 RT eukaryotic expression.";  
 RL Nucleic Acids Res. 13:4417-4429(1985).  
 RN [5]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=87298639; PubMed=3040015;  
 RA Shakhov A.N., Nedospasov S.A.;  
 RT "Molecular cloning of genes coding for tumor necrosis factor.  
 RT Complete nucleotide sequence of the genome copy of TNF-alpha in  
 RT mice.";  
 RL Bioorg. Khim. 13:701-705(1987).  
 RN [6]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=88067722; PubMed=3684584;  
 RA Senon D., Kawashima E., Jongeneel C.V., Shakhov A.N., Nedospasov S.A.;  
 RA Ikegami H., Makino S., Yamato E., Kawaguchi Y., Ueda H., Sakamoto T.,  
 RA Takekawa K., Ogiwara T.;  
 RT "Identification of a new susceptibility locus for insulin-dependent  
 RT diabetes mellitus by ancestral haplotype congenic mapping.";  
 RL J. Clin. Invest. 96:1936-1942(1995).  
 RN [8]  
 RN SEQUENCE OF 80-99.  
 RX MEDLINE=91097531; PubMed=2268312;  
 RA Sherry B., Juc D.-M., Zentella A., Cerami A.;  
 RA "Characterization of high molecular weight glycosylated forms of  
 RA murine tumor necrosis factor.";  
 RL Biochem. Biophys. Res. Commun. 173:1072-1078(1990).  
 RN [9]  
 RN SEQUENCE OF 70-87.  
 RX MEDLINE=89380231; PubMed=2777790;  
 RA Cseh K., Beutler B.;  
 RA "Alternative cleavage of the cachectin/tumor necrosis factor  
 RA propeptide results in a larger, inactive form of secreted protein.";  
 RL J. Biol. Chem. 264:16256-16260(1989).  
 RN [10]  
 RN IDENTIFICATION OF MEMBRANE-BOUND FORM.  
 RX MEDLINE=88165056; PubMed=3349526;  
 RA Kriegler M., Perez X., Defay K., Albert I., Lu S.D.;  
 RA "A novel form of TNF/cachectin is a cell surface cytotoxic  
 RA transmembrane protein: ramifications for the complex physiology of  
 RA TNF.";  
 RL Cell 53:45-53(1988).  
 RN [11]  
 RN X-RAY CRYSTALLOGRAPHY (1.4 ANGSTROMS) OF 80-235.  
 RX MEDLINE=99190964; PubMed=10089307;

RA Baeyens K.J., De Bondt H.L., Raeymaekers A., Fiers W., De Ranter C.J.;  
 RT "The structure of mouse tumour-necrosis factor at 1.4 A resolution:  
 RT towards modulation of its selectivity and trimerization.";  
 RL Acta Crystallogr. D 55:772-778(1999).  
 CC -!- FUNCTION: TNF IS MAINLY SECRETED BY MACROPHAGES, IT IS A CYTOKINE  
 CC WITH A WIDE VARIETY OF FUNCTIONS: IT CAN CAUSE CYTOLYSIS OF  
 CC CERTAIN TUMOR CELL LINES, IT IS IMPLICATED IN THE INDUCTION OF  
 CC CACHEXIA, IT IS A POTENT PYROGEN CAUSING FEVER BY DIRECT ACTION  
 CC OR BY STIMULATION OF INTERLEUKIN 1 SECRETION, IT CAN STIMULATE  
 CC CELL PROLIFERATION AND INDUCE CELL DIFFERENTIATION UNDER CERTAIN  
 CC CONDITIONS.  
 CC -!- SUBUNIT: HOMOTRIMER.  
 CC -!- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS AN  
 CC EXTRACELLULAR SOLUBLE FORM.  
 CC -!- PTM: THE SOLUBLE FORM DERIVES FROM THE MEMBRANE FORM BY  
 CC PROTEOLYTIC PROCESSING.  
 CC -!- DISEASE: CACHEXIA ACCOMPANIES A VARIETY OF DISEASES, INCLUDING  
 CC CANCER AND INFECTION, AND IS CHARACTERIZED BY GENERAL ILL HEALTH  
 CC AND MALNUTRITION.  
 CC -!- SIMILARITY: BELONGS TO THE TUMOR NECROSIS FACTOR FAMILY.  
 CC -----  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC -----  
 DR EMBL; U06950; AAA18594.1; -;  
 DR EMBL; M13049; AAA40457.1; -;  
 DR EMBL; M11731; AAA40458.1; -;  
 DR EMBL; Y00467; CAA68530.1; -;  
 DR EMBL; X02611; CAA28457.1; -;  
 DR EMBL; M20155; AAA40462.1; ALT\_SEQ.  
 DR EMBL; M38296; AAA40459.1; -;  
 DR EMBL; D84196; BAA19512.1; -;  
 DR EMBL; D84194; BAA19512.1; JOINED.  
 DR EMBL; D84195; BAA19512.1; JOINED.  
 DR EMBL; D84199; BAA19513.1; -;  
 DR EMBL; D84197; BAA19513.1; JOINED.  
 DR EMBL; D84198; BAA19513.1; JOINED.  
 DR PIR; A23127; QWMSN.  
 DR PIR; A22908; A22908.  
 DR PIR; A25164; A25164.  
 DR PIR; A27303; A27303.  
 DR PIR; A34251; A34251.  
 DR PIR; S03791; S03791.  
 DR PDB; 2TNF; 12-OCT-99.  
 DR MGD; MGI:104798; Tnf.  
 DR InterPro; IPR000478; Tnf.  
 DR InterPro; IPR002959; -;  
 DR Pfam; PF00229; TNF; 1.  
 DR PRINTS; PR01234; TNECROSISFCT.  
 DR PRINTS; PR01235; TNFALPHA.  
 DR PROSITE; PS00251; TNF\_1; 1.  
 DR PROSITE; PS50049; TNF\_2; 1.  
 KW Cytokine; Cytotoxin; Transmembrane; Glycoprotein; Signal-anchor;  
 KW 3D-structure.  
 FT PROPEP 1 79  
 FT CHAIN 80 235  
 FT TRANSMEM 36 56  
 FT DISULFID 148 179  
 FT CARBOHYD 86 86  
 FT CONFLICT 231 231  
 SQ SEQUENCE 235 AA; 25895 MW; 16DD2A9676D68C5D CRC64;  
 G -> R (IN REF. 3 AND 4).  
 N-LINKED (GLCNAC...)  
 TUMOR NECROSIS FACTOR.  
 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN).  
 Query Match 7.6% Score 85; DB 1; Length 235;  
 Best Local Similarity 23.0% Pred. No. 0.64; Indels 36; Gaps 8;  
 Matches 46; Conservative 31; Mismatches 87;  
 QY 18 SYFYLTATLALCLVFTVATIMVLVQRTSDIPNSPNVPLKGGNCSEDLICILKRAPFK 77



A;Title: CD30 antigen, a marker for Hodgkin's lymphoma, is a receptor whose ligand de  
A;Reference number: A40710; MUID:93313964  
A;Accession: B40710

A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-239 <SMI>  
A:Cross-references: GB:L09754; NID:g349288; PIDN:AAA74595.1; PID:g349289  
C:Keywords: cytokine receptor; membrane protein; surface antigen

Query Match 72.9%; Score 814.5; DB 2; Length 239;  
Best Local Similarity 70.6%; Pred. No. 1.2e-69;  
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

Qy 1 MHVPAGSVAS-----HLGTTSSRYFLTTATLALCLVFTVATIMVLVQRTDSIPNSPD 54

Db 20 MQVQPGSVASPWRSRPRWRSTSRSYFLSTTAL-VCLVAVAILVLVYQKDKSTPNTTE 78

Qy 55 NVPLKGGNCSEDLILKRAPKSWAYLOVAKHLNKTLSNKKDGLIHGVRYQDGNLVI 114

Db 79 KAPLKGNCSEDLFTLKTSPKSWAYLQVSKHLNNTKLSWNEDGTIRGLIYQDGNLIV 138

Qy 115 QPGLYFICQLQFLVQCPNNSVDLKLLELNKHTKQALVTVCSGMOTKHVYQNLQSF 174

Db 139 QPGLYFIVCQLQFLVQCSNHSVDLTQLLINSKIKKQTLVTVCSGVSKNIYQNLQSF 198

Qy 175 LLDYLVQNTTISVNVDTFYIDTSTFPLENVLISFIYNSND 215

Db 199 LLHYLVQNTTISVRVDNFQYVDNTFPLDNLVSLVLYSSSD 239

RESULT 3

A53062

Fas ligand - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 05-Nov-1999

R:Takanashi, T.; Tanaka, M.; Brannan, C.I.; Jenkins, N.A.; Copeland, N.G.; Suda, T.; Nag

Cell 76, 969-976, 1994

A:Title: Generalized lymphoproliferative disease in mice, caused by a point mutation in

A:Reference number: A53062; MUID:94185175

A:Accession: A53062

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-279 <TAK>

A:Cross-references: GB:U06948; NID:g473564; PIDN:AAA17800.1; PID:g473565

Query Match 10.0%; Score 112; DB 2; Length 279;

Best Local Similarity 22.6%; Pred. No. 0.0043;

Matches 38; Conservative 30; Mismatches 58; Indels 42; Gaps 6;

Qy 33 FTVATIMVLVYQRTDSIPNSPDVPLKGGNCSEDLILKRAPKSWAYLOVAKHLNKT 92

Db 115 FTNQLKVSSEFKQIANSTPSE-----KKEP--RSVAHLTGPHRSRI 156

Qy 93 KLSNWK---DGILHGVRYQDGNLVIQFPGLYFIICQLQFLVQ-CPNNSVDLKLLELNKH 148

Db 157 PLEWDYTGALISGKYKKGVLINERGLYFVSKVYFRGQSCNQPLNHHKVMRNSKY 216

Qy 149 -----IKKQALVTVCSGM-----OTKHVYQNLQSFLL 176

Db 217 PEDLVLMEEKRLNCTTGQIWAHSSYLGAVFNLTSAHDLYVNIQSLSL 264

RESULT 4

JQ1344

tumor necrosis factor alpha precursor - horse

N:Alternate names: cachectin; TNF alpha

C:Species: Equus caballus (domestic horse)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000

R:Su, X.; Morris, D.D.; McGraw, R.A.

Gene 107, 319-321, 1991

A:Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis

A:Reference number: JQ1344; MUID:92084125

A:Accession: JQ1344

A:Molecule type: DNA

A:Residues: 1-234 <SUX>

A:Cross-references: GB:M64087; NID:g164244; PIDN:AAA30959.1; PID:g164245

C:Comment: This protein is an important proximal mediator of endotoxemia.

C:Genetics:

A:Gene: TNF-alpha

A:Introns: 62/3; 79/1; 95/1

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine, cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; m

F:19,20/Binding site: myristate (lys) (covalent) #status predicted

F:82/Binding site: carboxylate (Ser) (covalent) #status predicted

F:146-178/Disulfide bonds: #status predicted

Query Match 8.6%; Score 96.5; DB 1; Length 234;

Best Local Similarity 24.7%; Pred. No. 0.1;

Matches 48; Conservative 33; Mismatches 88; Indels 25; Gaps 8;

Qy 18 SYFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDVPLKGGNCSEDLILKRAPFK 77

Db 37 SFLLVAGATTFLCLH----FGVIGPOREBPOLNFAQSI-----NPLAQTLRSSRTPSD 87

Qy 78 KSWAYLOVAKHLNKTLSW---NKDGIL-HGVRYQDGNLVIQFPGLYFIICQLQFLVQ-C 132

Db 88 KPAHV-VANPQAEQQLWLSGRANALLANGVKLTDLNQLVPLDGLYLYSQVLKGGGC 146

Qy 133 PNNSVDL--KLELLINKHKQALVTVCSGMQT-----KHVYQNLQSFLLDYLVQVN 182

Db 147 PSTHVLTLTISRLAVSPKSVNLLSAIKSPCHTESPEQAEAKPWEPYILGGVFOLEKG 206

Qy 183 TTISVNVDTFYQID 196

Db 207 DQLSAEINQPNYLD 220

RESULT 5

I54490

tumor necrosis factor alpha precursor - white-footed mouse

C:Species: Peromyscus leucopus (white-footed mouse)

C:Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 04-Feb-2000

A:Accession: I54490

R:Crew, M.D.; Filipowsky, M.E.

Immunogenetics 35, 351-353, 1992

A:Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus l

A:Reference number: I54490; MUID:92218012

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-235 <RES>

A:Cross-references: GB:M59233; NID:g202506; PIDN:AAA40596.1; PID:g202507

C:Genetics:

A:Gene: TNF

A:Introns: 62/3; 81/1; 97/1

C:Superfamily: tumor necrosis factor

C:Keywords: glycoprotein; lipoprotein; myristylation

F:19,20/Binding site: myristate (lys) (covalent) #status predicted

F:84/Binding site: carboxylate (Ser) (covalent) #status predicted

Query Match 8.4%; Score 94; DB 2; Length 235;

Best Local Similarity 24.0%; Pred. No. 0.18;

Matches 48; Conservative 31; Mismatches 85; Indels 36; Gaps 8;

Qy 18 SYFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDVPLKGGNCSEDLILKRAPFK 77

Db 37 SFLLVAGATTFLCLH----NFGVIGPOREBPOLNFAQSI-----NPLIIGSMAQTLTLRSSSSQSSD 89

Qy 78 KSWAYLOVAKHLNKTLSWKNKG-----ILHGVRYQDGNLVIQFPGLYFIICQLQFLVQ-C 132

Db 90 KPAHV-VANHQVDEQLEWLSRGANALLANGMDLKNQLVLPADGLYLYSQVLKGGGC 148

[illegible]



```

||||| :|| :|| ||| : :|| | :||| ||| :||| |||
Db 461 LALACSADSVAFPVLTSTHSTRGLPDTDPE-----DNEIVCFLK-----VQIA 502

Qy 87 KHLNKTLSLWNKDGTLGHVRVDGNGLVTFPCLYFIICQLQFLYQCPSNVSDLKLELLIN 146
      : :| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 503 EAIN-----LQDKNLMAQLQETMRCVCRF-----DNRTCRLKLASIA 539

Qy 147 KHIIKKQ----ALVTVCESGMOT--KHVYQNLSQFLLDYLVQN---TTISVN----- 188
      : :| :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 540 EDYRKRPAYIALFTCRGLOTTQAHLERLQRVLDRDEVANRYFTTVCVRLLLESKEKK 599

Qy 189 ----VDTFQYI----DTSTFFPLENVLSIFLY 211
      : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||
Db 600 IREFIQDFOKLTAADDKTAQVEDFLQ-ELY 628

RESULT 11
A49266
fas ligand - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: A49266
R:Suda, T.; Takahashi, T.; Golstein, P.; Nagata, S.
Cell 75, 1169-1178, 1993
A>Title: Molecular cloning and expression of the Fas ligand, a novel member of the tumor necrosis factor gene family
A:Reference number: A49266; MUID:94084792
A:Accession: A49266
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-278 <SUD>
A:Cross-references: GB:U03470; NID:g440178; PIDN:AAC52129.1; PID:g440179
C:Keywords: glycoprotein; transmembrane protein
```

	Query Match	7.7%; Score 86; DB 2; Length 278;	
	Best Local Similarity 23.6%; Pred. No. 1.2;		
	Matches 29; Conservative 21; Mismatches 49; Indels 24; Gaps 4;		
QY	78 KSWAYIQVAKHLNKTLSWNK---DGILHGVRYYODGNLVIOFPGLYFIFICQLVLVQ-CP	133	: : : :      : : : :            : : : :
Dd	141 RSV AHLTG NPRSIPLEWEDTY TALISGVKKYKKG LVLVINEAGLYFYSKVYPRGOSCN	200	: : : :      : : : :            : : : :
QY	134 NNSVDLKLLELLINKH-----IKKALVTVCESGM-----QTKHVVQNLSQ	173	: : : :      : : : :            : : : :
Dd	201 SQPSLSHKVVMRFNFXYPGDLVLMEEKKLNCTTGTQIWAHS SYLGAVFNLTVA DHLYVNISQ	260	: : : :      : : : :            : : : :
QY	174 FLL 176		
Dd	261 I.S.L. 263		

Db 261 LSL 263

RESULT 12  
I53384  
4-1BB ligand - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C:Accession: I53384  
R:Goodwin, R.G.; Din, W.S.; Davis-Smith, T.; Anderson, D.M.; Gimpel, S.D.; Sato, T.A.  
Eur. J. Immunol. 23, 2631-2641, 1993  
A:Title: Molecular cloning of a ligand for the inducible T cell gene 4-1BB: a member  
A:Reference number: I53384; MUID:94009225  
A:Accession: I53384  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-309 <RES>  
A:Cross-references: GB:I515435; NID:q435996; PIDN:AAA39435.1; PID:q435997

Query Match 7.6%; Score 85.5; DB 2; Length 309;  
Best Local Similarity 23.5%; Pred. No. 1.6;  
Matches 52; Conservative 38; Mismatches 78; Indels 53; Gaps 12;  
QY 27 LALCLVETVATIMVLVYVORTDISP-----NSPDNV-PLKGGNCSEDLICIL 71

A::Title: Identification of a common nucleotide sequence in the 3'-untranslated region  
A::Reference number: I59058; MUID:86149365  
A::Accession: I59058  
A::Status: preliminary; translated from GB/EMBL/DDBJ  
A::Molecule type: mRNA  
A::Residues: 1-230,'R',232-235 <RES>  
A::Cross-references: GB:M13049; NID:g202082; PIDN:AAA40457.1; PID:g202083  
R::Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.  
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990  
A::Title: Characterization of high molecular weight glycosylated forms of murine tumor  
F::Binding site: carbohydrate (Ser) (covalent) #status predicted  
F::Binding site: carbohydrate (Asn) (covalent) #status predicted  
F::Disulfide bonds: #status predicted

Query Match                7.6%     Score 85;   DB 1; Length 235;  
Best Local Similarity    23.08; Pred No. 1.3;  
Matches      46; Conservative                87; Indels    36; Gaps    8;

Qy 18 SYFYTTATLALCLVFTVATIMLVLTGRTSDIPNSPDNVPLKGGNCSEDLILCLKRAPFK 77  
| : : || || | : : || : || : ||  
Db 37 SFLLVAGATTFLC||---NFGVIGPQRDEKFPN---GLPLISSMAQTTLTRSSSQNSSD 89  
| : : || || | : : || : || : ||  
Qy 78 KSWAYLQVAKHLNKTSLWNKDG-----ILHGVRYQDNVLVIQFGLYFIICQLQFLVQ-C 132  
| : : || : : || : || : || : || : || : || : || : || : || : || : || : || : ||  
Db 90 KPVAHV-VANHQVEQELEWLSQRSANALLANGMDLKQLVVPADGLYLVTYSQVLFKGGC 148  
| : : || : : || : || : || : || : || : || : || : || : || : || : || : || : ||  
Qy 133 PNN-----SVDLKLELLINKHQALVTVC----ESGMOTKHVYNLSQFL 176  
| : : || : || : || : || : || : || : || : || : || : || : || : || : || : ||  
Db 149 PDYVLLHTVSFRFAISVQEKVNLL-----SAVKSPCKDTPEGAEKLPWEPIYLGCV 201  
| : : || : || : || : || : || : || : || : || : || : || : || : || : || : ||  
Qy 177 DYLVNTTISVNDTFQYID 196  
| : : || : || : || : || : || : || : || : || : || : || : || : || : || : ||  
Db 202 FOLEKGDSLAEVNLPKYLD 221  
| : : || : || : || : || : || : || : || : || : || : || : || : || : || : ||

RESULT 14  
S12606  
tumor necrosis factor alpha precursor - pig  
C::Species: Sus scrofa domestica (domestic pig)  
C::Date: 10-Sep-1999 #sequence.revision 10-Sep-1999 #text\_change 04-Feb-2000  
C::Accession: S12606; S17290; S18965; I46659  
R::Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.  
Nucleic Acids Res. 18, 5564, 1990  
A::Title: Gene sequence of porcine tumor necrosis factor alpha.  
A::Reference number: S12606; MUID:91016861  
A::Accession: S12606  
A::Molecule type: DNA  
A::Residues: 1-232 <DRE>  
A::Cross-references: EMBL:X54001; NID:g2135; PIDN:CAA37949.1; PID:g2136  
R::Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.  
Gene 102, 171-178, 1991  
A::Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative  
A::Reference number: S17289; MUID:91340150  
A::Accession: S17290  
A::Molecule type: DNA  
A::Residues: 1-232 <KU>  
A::Cross-references: EMBL:X54859; NID:g2132; PIDN:CAA38639.1; PID:g2134  
A::Note: the authors translated the codon GAC for residue 202 as Gly  
R::Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P.  
submitted to the EMBL Data Library, January 1991  
A::Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis

A:Reference number: S18965

A:Accession: S18965

A:Molecule type: mRNA

A:Residues: 1-232 <CHO>

A:Cross-references: EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID:g2138

R:Pauli, U.; Beutler, B.; Peterhans, E.

Gene 81, 185-191, 1989

A:Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reaction

A:Reference number: I46659; MUID:90034181

A:Accession: I46659

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 44-232 <PAU>

A:Cross-references: GB:M29079; NID:g164694; PIDN:AAA31128.1; PID:g164695

C:Genetics:

A:Introns: 62/3; 78/1; 93/1

C:Superfamily: tumor necrosis factor

C:Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; myrl

F:1-77/Domain: propeptide #status predicted <PRO>

F:78-232/Product: tumor necrosis factor alpha #status predicted <MAT>

F:19,20/Binding site: myristate (Lys) (covalent) #status predicted

F:81/Binding site: carboxylate (Ser) (covalent) #status predicted

F:144-176/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 7.6%; Score 84.5; DB 1; Length 232;

Matches 45; Conservative 35; Mismatches 79; Indels 43; Gaps 9;

QY 18 SYFYLTATLALCLVFTVATIMLVVQRTDSIPNSPDV-PLKGGNCSEDLCLIKRAPF 76

DB 37 SFLVAGATTFLCLH- - - - -FEVIGPQKEFPAGPLSINPLAQGLRSS- - - - -QTS 84

QY 77 KKSWAYLOVAKHLNKTLSWKNKG- - - - -ILHGVRVODGNLVIOFPGLYFIICLOQLVQ- 131

DB 85 DRPVAHV-VANVKAEGQLQWQSYANALLANGVKLDNOLVPTDGLYLYYSQVLFRRGQ 143

QY 132 CPNNVVDL- - - - -KLELLINKHIKKQALVTVC- - - - -SGMOTKHVYQNLISQF 174

DB 144 CPSTNVFLTHTISRTAVSVQTKVNL- - - - -SAIKSPCQRETPGEAKPWYEPYILG 196

QY 175 LLDYLVQNTTISVNVDTFOYID 196

DB 197 GVFOLEKGDRLSAEINLPDYLD 218

RESULT 15

JH0529

tumor necrosis factor alpha precursor - sheep

N:Alternate names: cachectin; TNF alpha

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 04-Feb-2000

R:Accession: JH0529; S48118; S13114; S20661

R:Green, I.R.; Sargan, D.R.

Gene 109, 203-210, 1991

A:Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems with

A:Reference number: JH0529; MUID:92112044

A:Accession: JH0529

A:Molecule type: mRNA

A:Residues: 1-234 <GRE>

A:Cross-references: EMBL:X55152; NID:g1405; PIDN:CAA38952.1; PID:g1406

A:Experimental source: alveolar macrophage

R:Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E.

Immunol. Cell Biol. 69, 273-283, 1991

A:Title: Molecular cloning, expression and characterization of ovine TNF-alpha.

A:Reference number: S48118; MUID:92155784

A:Accession: S48118

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-234 <NAS>

A:Cross-references: EMBL:X56756; NID:g297806; PIDN:CAA40076.1; PID:g297807

R:Young, A.J.; Hay, J.B.; Chan, J.Y.C.

Nucleic Acids Res. 18, 6723, 1990

A:Title: Primary structure of ovine tumor necrosis factor alpha cDNA.

A:Reference number: S13114; MUID:91067496

A:Accession: S13114

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-62,64-234 <YOU>

A:Cross-references: EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:g1404

A:Note: comparison with the introns of homologous sequences suggest that this is prob

C:Superfamily: tumor necrosis factor

C:Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein; lym

F:1-77/Domain: propeptide #status predicted <PRO>

F:78-234/Product: tumor necrosis factor alpha #status predicted <TUM>

F:20/Binding site: myristate (Lys) (covalent) #status predicted

F:82/Binding site: carboxylate (Ser) (covalent) #status predicted

F:96/Binding site: carboxylate (Asn) (covalent) #status predicted

F:146-178/Disulfide bonds: #status predicted

Query Match

Best Local Similarity 7.5%; Score 83.5; DB 1; Length 234;

Matches 47; Conservative 29; Mismatches 85; Indels 41; Gaps 9;

QY 18 SYFYLTATLALCLVFTVATIMLVVQRTDSIPNSPD-NVPLKGGNCSEDLCLIKRAPF 76

DB 37 SFLVAGATTFLCLH- - - - -FGVIGPQREEQSPAGSFNRPL- - - - -VQTLRSSQASN 86

QY 77 KKSWAYLOVAKHLNKTLSWKNKG- - - - -ILHGVRVODGNLVIOFPGLYFIICLOQLVQ- 131

DB 87 NKPAHV-VANISAPQLRWGDSYANALMANGVELKDNOLVPTDGLYLYYSQVLFRRHG 145

QY 132 CPNN- - - - -SVDLKLLELLINKHIKKQALVTVC- - - - -SGMOTKHVYQNLISQF 174

DB 146 CPSTPLFLTHTISRTAVSVQTKVNL- - - - -SAIKSPCHRETLGAEAKPWYEPYIQG 198

QY 175 LLDYLVQNTTISVNVDTFOYID 196

DB 199 GVFOLEKGDRLSAEINLPDYLD 220

Search completed: September 5, 2001, 10:23:53

Job time: 123 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2001, 10:23:11 ; Search time 25.09 seconds  
(without alignments)  
176.442 Million cell updates/sec

Title: US-09-628-126-23  
Perfect score: 1118  
Sequence: 1 MHPAGSVASHLGTTSRSYF.....DTSTFPLENVLISFLYSNSD 215

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Total number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued Patents.AA.\*  
1: /cgn2\_6/ptodata/2/iaa/5A-COMB.pep.\*  
2: /cgn2\_6/ptodata/2/iaa/5B-COMB.pep.\*  
3: /cgn2\_6/ptodata/2/iaa/6A-COMB.pep.\*  
4: /cgn2\_6/ptodata/2/iaa/6B-COMB.pep.\*  
5: /cgn2\_6/ptodata/2/iaa/PCTUS-COMB.pep.\*  
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1118	100.0	215	1 US-08-225-989-23	Sequence 23, Appl
2	1118	100.0	215	1 US-08-570-923-23	Sequence 23, Appl
3	1118	100.0	215	1 US-08-580-014-23	Sequence 23, Appl
4	1118	100.0	215	4 US-09-079-785-23	Sequence 23, Appl
5	1118	100.0	234	1 US-08-225-989-8	Sequence 8, Appl
6	1118	100.0	234	1 US-08-570-923-8	Sequence 8, Appl
7	1118	100.0	234	1 US-08-580-014-8	Sequence 8, Appl
8	1118	100.0	234	4 US-09-079-785-8	Sequence 8, Appl
9	814.5	72.9	220	1 US-08-225-989-19	Sequence 19, Appl
10	814.5	72.9	220	1 US-08-570-923-19	Sequence 19, Appl
11	814.5	72.9	220	1 US-08-580-014-19	Sequence 19, Appl
12	814.5	72.9	220	4 US-09-079-785-19	Sequence 19, Appl
13	814.5	72.9	239	1 US-08-225-989-6	Sequence 6, Appl
14	814.5	72.9	239	1 US-08-570-923-6	Sequence 6, Appl
15	814.5	72.9	239	1 US-08-580-014-6	Sequence 6, Appl
16	814.5	72.9	239	4 US-09-079-785-6	Sequence 6, Appl
17	775	69.3	148	3 US-08-584-031-12	Sequence 12, Appl
18	592	53.0	125	1 US-08-225-989-20	Sequence 20, Appl
19	592	53.0	125	1 US-08-570-923-20	Sequence 20, Appl
20	592	53.0	125	1 US-08-580-014-20	Sequence 20, Appl
21	592	53.0	125	4 US-09-079-785-20	Sequence 20, Appl
22	447.5	40.0	130	1 US-08-225-989-21	Sequence 21, Appl
23	447.5	40.0	130	1 US-08-570-923-21	Sequence 21, Appl
24	447.5	40.0	130	1 US-08-580-014-21	Sequence 21, Appl
25	447.5	40.0	130	4 US-09-079-785-21	Sequence 21, Appl
26	274	24.5	52	4 US-09-369-494-17	Sequence 17, Appl
27	102	9.1	279	5 PCT-US95-00362-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1  
US-08-225-989-23  
; Sequence 23, Application US/08225989  
; Patent No. 5480981  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644

Sequence 21, Appl  
Sequence 8, Appl  
Sequence 5, Appl  
Sequence 9, Appl  
Sequence 2, Appl  
Sequence 2, Appl  
Sequence 25, Appl  
Sequence 3, Appl  
Sequence 2, Appl  
Sequence 16, Appl  
Sequence 17, Appl  
Sequence 99, Appl  
Sequence 2, Appl  
Sequence 61, Appl  
Sequence 60, Appl  
Sequence 64, Appl  
Sequence 7, Appl  
Sequence 43, Appl

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 889,717
; FILING DATE: 26-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2804-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-570-923-23

Query Match      100.0%; Score 1118; DB 1; Length 215;
Best Local Similarity 100.0%; Pred. No. 5.9e-114;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY   1  MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVVQRTDSIPNSPDNVPLKG 60
     |||||
Db    1  MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVVQRTDSIPNSPDNVPLKG 60

QY   61  GNCSEDLLCILKRAPFKSWAYLQVAKHLNKTLSWNKDGILHGVRVDGGLNLVTQFPGLY 120
     |||||
Db    61  GNCSEDLLCILKRAPFKSWAYLQVAKHLNKTLSWNKDGILHGVRVDGGLNLVTQFPGLY 120

QY   121  FITCOLQLVQCNPNSVDLKLELLINKHKQAALTVCESGMQRKHVYONLSQFLLDYLQ 180
     |||||
Db    121  FITCOLQLVQCNPNSVDLKLELLINKHKQAALTVCESGMQRKHVYONLSQFLLDYLQ 180

QY   181  VNTTISVNDFTFQYIDTFSTFPLENVLSIFLYSNSD 215
     |||||
Db    181  VNTTISVNDFTFQYIDTFSTFPLENVLSIFLYSNSD 215

RESULT          3
US-08-580-014-23
; Sequence 23, Application US/08580014
; Patent No. 5753203
; GENERAL INFORMATION:
; APPLICANT: Goodwin, Raymond G.
; APPLICANT: Smith, Craig A.
; APPLICANT: Armitage, Richard J.
; APPLICANT: Gruss, Hans-Jurgen
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,014
; FILING DATE: 20-DEC-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/225,989
; FILING DATE: 12 APRIL 1994
; APPLICATION NUMBER: US 07/966,775
; FILING DATE: 27-OCT-1992
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CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 215 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-580-014-23

Query Match 100.0%; Score 1118; DB 1; Length 215;  
Best Local Similarity 100.0%; Pred. No. 5.9e-114;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLKG 60  
Db 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLKG 60  
Qy 61 GNCSEDLCLILKRAPPKKSWAYLQVAKHLNKTLSNKGILHGVRYQDGNLVLPGLY 120  
Db 61 GNCSEDLCLILKRAPPKKSWAYLQVAKHLNKTLSNKGILHGVRYQDGNLVLPGLY 120  
Qy 121 FIICQLQFLVQCPNNSVDLKLKLELLINKHKKQALVTVCESGMOTKHVYQNLVSQFLLDYLQ 180  
Db 121 FIICQLQFLVQCPNNSVDLKLKLELLINKHKKQALVTVCESGMOTKHVYQNLVSQFLLDYLQ 180  
Qy 181 VNTTISVNVDTFOYIDTSTFFPLENVLSIFLYNSND 215  
Db 181 VNTTISVNVDTFOYIDTSTFFPLENVLSIFLYNSND 215

RESULT 4  
US-09-079-785-23  
Sequence 23, Application US/09079785  
Patent No. 6143869  
GENERAL INFORMATION:  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
APPLICANT: Armitage, Richard J.  
APPLICANT: Gruss, Hans-Jurgen  
TITLE OF INVENTION: NO. 6143869el Cytokine That Binds CD30  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1

SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/079,785  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,989  
FILING DATE: 12 APRIL 1994  
APPLICATION NUMBER: US 07/966,775  
FILING DATE: 27-OCT-1992  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 215 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-079-785-23

Query Match 100.0%; Score 1118; DB 4; Length 215;  
Best Local Similarity 100.0%; Pred. No. 5.9e-114;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLKG 60  
Db 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLKG 60  
Qy 61 GNCSEDLCLILKRAPPKKSWAYLQVAKHLNKTLSNKGILHGVRYQDGNLVLPGLY 120  
Db 61 GNCSEDLCLILKRAPPKKSWAYLQVAKHLNKTLSNKGILHGVRYQDGNLVLPGLY 120  
Qy 121 FIICQLQFLVQCPNNSVDLKLKLELLINKHKKQALVTVCESGMOTKHVYQNLVSQFLLDYLQ 180  
Db 121 FIICQLQFLVQCPNNSVDLKLKLELLINKHKKQALVTVCESGMOTKHVYQNLVSQFLLDYLQ 180  
Qy 181 VNTTISVNVDTFOYIDTSTFFPLENVLSIFLYNSND 215  
Db 181 VNTTISVNVDTFOYIDTSTFFPLENVLSIFLYNSND 215  
RESULT 5  
US-08-225-989-8  
Sequence 8, Application US/08225989  
Patent No. 5480981  
GENERAL INFORMATION:  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
APPLICANT: Armitage, Richard J.  
APPLICANT: Gruss, Hans-Jurgen  
TITLE OF INVENTION: NO. 5480981el Cytokine That Binds CD30  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,989  
FILING DATE: 12 APRIL 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/966,775  
FILING DATE: 27-OCT-1992  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 234 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-225-989-8

Query Match 100.0%; Score 1118; DB 1; Length 234;  
Best Local Similarity 100.0%; Pred. No. 6.6e-114;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVPLKG 60  
|||||  
DB 20 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVPLKG 79  
|||||  
QY 61 GNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSWNKDGILHGVRQDGNLVIQPPGLY 120  
|||||  
DB 80 GNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSWNKDGILHGVRQDGNLVIQPPGLY 139  
|||||  
QY 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKQALVTVCESGMQTKHYQNLQSOFLLDYIQ 180  
|||||  
DB 140 FIICQLQFLVQCPNNSVDLKLLELLINKHKQALVTVCESGMQTKHYQNLQSOFLLDYIQ 199  
|||||  
QY 181 VNTTISVNDVTFQYIDTSTFPLENVLSIFLYSNSD 215  
|||||  
DB 200 VNTTISVNDVTFQYIDTSTFPLENVLSIFLYSNSD 234  
|||||

## RESULT 6

US-08-570-923-8  
; Sequence 8, Application US/08570923  
; Patent No. 5677430

GENERAL INFORMATION:  
APPLICANT: Goodwin, Raymond G.  
APPLICANT: Smith, Craig A.  
APPLICANT: Armitage, Richard J.  
APPLICANT: Gruss, Hans-Jurgen  
TITLE OF INVENTION: No. 5677430el Cytokine That Binds CD30  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/570,923  
FILING DATE: 12-DEC-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/225,989  
FILING DATE: 12 APRIL 1994  
APPLICATION NUMBER: US 07/966,775  
FILING DATE: 27-OCT-1992  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 907,224  
FILING DATE: 01-JUL-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 899,660  
FILING DATE: 15-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 892,459  
FILING DATE: 02-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 889,717  
FILING DATE: 26-MAY-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2804-E  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 234 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-570-923-8

Query Match 100.0%; Score 1118; DB 1; Length 234;  
Best Local Similarity 100.0%; Pred. No. 6.6e-114;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVPLKG 60  
|||||  
DB 20 MHVPAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVPLKG 79  
|||||  
QY 61 GNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSWNKDGILHGVRQDGNLVIQPPGLY 120  
|||||  
DB 80 GNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSWNKDGILHGVRQDGNLVIQPPGLY 139  
|||||  
QY 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKQALVTVCESGMQTKHYQNLQSOFLLDYIQ 180  
|||||  
DB 140 FIICQLQFLVQCPNNSVDLKLLELLINKHKQALVTVCESGMQTKHYQNLQSOFLLDYIQ 199  
|||||

QY 181 VNTTISVNDTFQYIDTSTFFPLENVLSIFLYSNSD 215  
Db 200 VNTTISVNDTFQYIDTSTFFPLENVLSIFLYSNSD 234

## RESULT 7

US-08-580-014-8  
; Sequence 8, Application US/08580014  
; Patent No. 5753203  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/580,014  
; FILING DATE: 20-DEC-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 234 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-580-014-8

Query Match 100.0%; Score 1118; DB 1; Length 234;  
Best Local Similarity 100.0%; Pred. No. 6.6e-114;  
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHPVAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVPLKG 60

Db 20 MHPVAGSVASHLGTTSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPDNVPLKG 79  
QY 61 GNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSNKNKGILHGVRYQDGNLVIQPPGLY 120  
Db 80 GNCSEDLICILKRAPFKKSWAYLQVAKHLNKTLSNKNKGILHGVRYQDGNLVIQPPGLY 139  
QY 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKKKALVTVCSGMQTKHYQNLQSFLLDYLO 180  
Db 140 FIICQLQFLVQCPNNSVDLKLLELLINKHKKKALVTVCSGMQTKHYQNLQSFLLDYLO 199  
QY 181 VNTTISVNDTFQYIDTSTFFPLENVLSIFLYSNSD 215  
Db 200 VNTTISVNDTFQYIDTSTFFPLENVLSIFLYSNSD 234  
RESULT 8  
US-09-079-785-8  
; Sequence 8, Application US/09079785  
; Patent No. 6143869  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 6143869el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/079,785  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989  
; FILING DATE: 12 APRIL 1994  
; APPLICATION NUMBER: US 07/966,775  
; FILING DATE: 27-OCT-1992  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 907,224  
; FILING DATE: 01-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 899,660  
; FILING DATE: 15-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 892,459  
; FILING DATE: 02-JUN-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 889,717  
; FILING DATE: 26-MAY-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Seese, Kathryn A.  
; REGISTRATION NUMBER: 32,172  
; REFERENCE/DOCKET NUMBER: 2804-E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (206)587-0430  
; TELEFAX: (206)233-0644  
; TELEX: 756822  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 234 amino acids  
; TYPE: amino acid





RESULT 11  
US-08-580-014-19  
; Sequence 19, Application US/08580014  
; Patent No. 5753203  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: No. 5753203el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: Apple Macintosh  
; OPERATING SYSTEM: Apple 7.1  
; SOFTWARE: Microsoft Word, Version 5.1a  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/580,014  
; FILING DATE: 20-DEC-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,989

RESULT 12  
US-09-079-785-19  
; Sequence 19, Application US/09079785  
; Patent No. 6143869  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen  
; TITLE OF INVENTION: NO. 6143869el Cytokine That Binds CD30  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
; STREET: 51 University Street  
; CITY: Seattle  
; STATE: Washington  
; COUNTRY: USA  
; ZIP: 98101  
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: Apple Macintosh  
;; OPERATING SYSTEM: Apple 7.1  
;; SOFTWARE: Microsoft Word, Version 5.1a  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/079,785  
;; FILING DATE:  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/225,989  
;; FILING DATE: 12 APRIL 1994  
;; APPLICATION NUMBER: US 07/966,775  
;; FILING DATE: 27-OCT-1992  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 907,224  
;; FILING DATE: 01-JUL-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 899,660  
;; FILING DATE: 15-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 892,459  
;; FILING DATE: 02-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 889,717  
;; FILING DATE: 26-MAY-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Seese, Kathryn A.  
;; REGISTRATION NUMBER: 32,172  
;; REFERENCE/DOCKET NUMBER: 2804-E  
;; TELEPHONE: (206)587-0430  
;; TELEFAX: (206)233-0644  
;; TELEX: 756822  
;; INFORMATION FOR SEQ ID NO: 19:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 220 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-09-079-785-19

Query Match 72.9%; Score 814.5; DB 4; Length 220;  
Best Local Similarity 70.6%; Pred. No. 6.5e-81;  
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;  
QY 1 MHVPAGSVAS-----HLGTTSSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPD 54  
Db 1 MQVQPGSVASPWRSRSTRPWRSTRSRSFYLTAL-VCLVAVAILVLVQKDKSTPNTTE 59  
QY 55 NVPLKGGNCSEDLCLILKRAPFKKSWAYLQVAKHLNKTLSNKGDLHGVRVQDGNLVI 114  
Db 60 KAPLKGNCSEDLCLILKRAPFKKSWAYLQVAKHLNKTLSNKGDLHGVRVQDGNLVI 119  
QY 115 QPPGLYFIICQLQFLVQCSPNNSVDLKLLELHINKKQALVTVCSGMOTKHVYQNLISQF 174  
Db 120 QPPGLYFIICQLQFLVQCSPNNSVDLKLLELHINKKQALVTVCSGMOTKHVYQNLISQF 179  
QY 175 LLDYLVQNTTISVNDVTFQYIDTSTFPFLENVLSIFLYSNSD 215  
Db 180 LLHYLVQNSTISVRVDFQYVDNTFPFLDNVLSVFLYSSSD 220

RESULT 13  
US-08-225-989-6  
; Sequence 6, Application US/08225989  
; Patent No. 5480981  
; GENERAL INFORMATION:  
; APPLICANT: Goodwin, Raymond G.  
; APPLICANT: Smith, Craig A.  
; APPLICANT: Armitage, Richard J.  
; APPLICANT: Gruss, Hans-Jurgen

;; TITLE OF INVENTION: No. 5480981el Cytokine That Binds CD30  
;; NUMBER OF SEQUENCES: 23  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Kathryn A. Seese, Immunex Corporation  
;; STREET: 51 University Street  
;; CITY: Seattle  
;; STATE: Washington  
;; COUNTRY: USA  
;; ZIP: 98101  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: Apple Macintosh  
;; OPERATING SYSTEM: Apple 7.1  
;; SOFTWARE: Microsoft Word, Version 5.1a  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/225,989  
;; FILING DATE: 12 APRIL 1994  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 07/966,775  
;; FILING DATE: 27-OCT-1992  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 907,224  
;; FILING DATE: 01-JUL-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 899,660  
;; FILING DATE: 15-JUN-1992  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 889,717  
;; FILING DATE: 26-MAY-1992  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Seese, Kathryn A.  
;; REGISTRATION NUMBER: 32,172  
;; REFERENCE/DOCKET NUMBER: 2804-E  
;; TELEPHONE: (206)587-0430  
;; TELEFAX: (206)233-0644  
;; TELEX: 756822  
;; INFORMATION FOR SEQ ID NO: 6:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 239 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; US-08-225-989-6

Query Match 72.9%; Score 814.5; DB 1; Length 239;  
Best Local Similarity 70.6%; Pred. No. 7.3e-81;  
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;  
QY 1 MHVPAGSVAS-----HLGTTSSRSFYLTATLALCLVFTVATIMVLVQRTDSIPNSPD 54  
Db 20 MQVQPGSVASPWRSRSTRPWRSTRSRSFYLTAL-VCLVAVAILVLVQKDKSTPNTTE 78  
QY 55 NVPLKGGNCSEDLCLILKRAPFKKSWAYLQVAKHLNKTLSNKGDLHGVRVQDGNLVI 114  
Db 79 KAPLKGNCSEDLCLILKRAPFKKSWAYLQVAKHLNKTLSNKGDLHGVRVQDGNLVI 138  
QY 115 QPPGLYFIICQLQFLVQCSPNNSVDLKLLELHINKKQALVTVCSGMOTKHVYQNLISQF 174  
Db 139 QPPGLYFIICQLQFLVQCSPNNSVDLKLLELHINKKQALVTVCSGMOTKHVYQNLISQF 198  
QY 175 LLDYLVQNTTISVNDVTFQYIDTSTFPFLENVLSIFLYSNSD 215  
Db 199 LLHYLVQNSTISVRVDFQYVDNTFPFLDNVLSVFLYSSSD 239

RESULT 14

Query Match	72.9%	Score 814.5	DB 1	Length 239;
Best Local Similarity	70.6%	pred. No. 7.3e-81;		
Matches	156;	Conservative	26;	Mismatches 32; Indels 7; Gaps 2;
Qy	1	MHVPGSVAS-----HIGTTSRSFYFTTTATLALCLVFTVTATIMLVVVQRTSDIPNSPD	54	
		:           :           :         :		
Db	20	MQVPGSVASPWRSTRPWRSTRSFYFLSTTAL-VCLVVAVAILLVVVQKDSPTNTE	78	
Qy	55	NVPLKGNCSEDLICILKRAPFKSWAYLOVAQHUNKTKLSWNKDGIUHGVRVQDGNLVI	114	
Db	79	KAPLKGGNCSEDLFCTJLKSTPSKSWAYLOVSKLHNTPKLSWNEOGTTHGLTYODGNLIV	138	

Query Match 72.9%; Score 814.5; DB 1; Length 239;  
Best Local Similarity 70.6%; Pred. No. 7.3e-81;

Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;

QY 1 MHVPAGSVAS-----HLGTTSSRYFLTATLALCLVFTVATIMVLVQRTDSIPNSPD 54  
 Db 20 MQVQPGSVASPRWSTPWRSTSRSYFLSTTAL-VCLVAVAILVLVQKKDSTPTTE 78  
 QY 55 NVPLKGGNCSEDLCLILKRAPPKSWAYLQVAKHLNKTLSWNKDGILHGVRVYQDGNLVI 114  
 Db 79 KAPLKGNCSEDLFCTLKSTPSKKSWAYLQVSKHLNNTKLSWNEDGTIHGLIYQDGNLIV 138  
 QY 115 QPGLYFIICQLQFLVQCPSNNSVDLKLLELLINKHIKKQALVTVCESGMQTKHVVQNLSQF 174  
 Db 139 QPGLYFIICQLQFLVQCPSNNSVDLTLQLLINSKIKKQTLVTVCESGVOSKNIYQNLSQF 198  
 QY 175 LLDYLVQVNTTISVNVDTFOYIDTSTFPLENVLSIFLYSNSD 215  
 Db 199 LLHYLVQVNTTISVNVDTFOYIDTSTFPLENVLSIFLYSNSD 239

Search completed: September 5, 2001, 10:23:11  
 Job time: 86 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 5, 2001, 10:22:39 ; Search time 44.86 Seconds  
(without alignments)  
290.552 Million cell updates/sec

Title: US-09-628-126-23  
Perfect score: 1118  
Sequence: 1 MHVPAGSVASHLGTTSRYP.....DTSTFPLENVLISFLYSNSD 215

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1118	100.0	215	14 AAR45007	Sequence encoded b
2	1118	100.0	234	14 AAR45009	Sequence encoded b
3	814.5	72.9	220	14 AAR45006	Sequence encoded b
4	814.5	72.9	239	14 AAR45008	Sequence encoded b
5	741	66.3	143	21 AAB08276	Amino acid sequenc
6	608	54.4	143	21 AAB08277	Amino acid sequenc
7	115	10.3	279	17 AAR88357	Mouse Fas ligand.
8	112	10.0	179	16 AAR79069	Mouse Fas ligand.
9	112	10.0	279	16 AAR79098	Mouse Fas ligand.
10	108	9.7	143	21 AAB08266	Amino acid sequenc
11	106	9.5	138	16 AAR79068	Mouse Fas ligand (

12	104	9.3	137	16	AAR79067	Mouse Fas ligand (
13	102	9.1	279	16	AAR77282	Mouse Fas-L protei
14	97	8.7	268	19	AAW48953	Non-cleavable Fas
15	96.5	8.6	265	19	AAW48954	Non-cleavable Fas
16	95	8.5	180	18	AAW10875	FasL/lt-alpha hybr
17	93	8.3	216	19	AAW68412	Hybrid alpha-1-thy
18	92	8.2	378	18	AAW35864	Human FasL-ligand: I
19	91.5	8.2	261	20	AAV28597	Fas ligand (FasL)
20	91.5	8.2	281	21	AAV87581	Human Fas ligand (
21	91.5	8.2	376	21	AAV52588	Secreted modified
22	91	8.1	258	20	AAV04371	C-terminally delet
23	90.5	8.1	145	18	AAW35848	Human Fas ligand d
24	90.5	8.1	151	18	AAW16667	Human Fas ligand f
25	90.5	8.1	178	16	AAR88308	Human Fas ligand (
26	90.5	8.1	179	16	AAR79099	C-terminally delet
27	90.5	8.1	179	18	AAW11814	Human Fas ligand (
28	90.5	8.1	271	20	AAV28596	Fas ligand. Homo
29	90.5	8.1	277	20	AAV28595	Fas ligand (FasL)
30	90.5	8.1	277	20	AAV04372	Fas ligand (FasL)
31	90.5	8.1	281	16	AAR77281	Human Fas ligand d
32	90.5	8.1	281	16	AAR79097	Human Fas-L protei
33	90.5	8.1	281	17	AAR98104	Human Fas ligand.
34	90.5	8.1	281	17	AAR88356	Human Fas ligand d
35	90.5	8.1	281	18	AAR27143	Human Fas ligand.
36	90.5	8.1	281	19	AAW75959	Human Fas ligand.
37	90.5	8.1	281	19	AAW49105	Human Fas ligand.
38	90.5	8.1	281	20	AAV28594	Wild type Fas liga
39	90.5	8.1	281	20	AAV04373	Fas Ligand. Mamma
40	90.5	8.1	281	20	AAW98071	Human Fas ligand d
41	90.5	8.1	281	20	AAW95041	Human Fas ligand (
42	90.5	8.1	281	20	AAW19342	Human FasL protein
43	90.5	8.1	281	21	AAV87569	Amino acid sequenc
44	90.5	8.1	281	21	AAV87576	Human Fas ligand (
45	90.5	8.1	281	21	AAV87577	Human Fas ligand (

#### ALIGNMENTS

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ID AAR45007 standard; Protein; 215 AA.  
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AC AAR45007;  
XX  
DT 19-JUN-1994 (first entry)  
XX  
DE Sequence encoded by a human CD30-L cDNA clone.  
XX  
KW Hodgkin's disease; lymphoma; surface antigen; cytokine;  
KW CD30 ligand; CD30-L; TNF; NGF.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Region 22..43  
FT /label= transmembrane  
XX  
FT  
XX  
PN W09324135-A.  
XX  
PD 09-DEC-1993.  
XX  
PF 25-MAY-1993; 93WO-US04926.  
XX  
PR 26-MAY-1992; 92US-0889717.  
PR 02-JUN-1992; 92US-0892459.  
PR 15-JUN-1992; 92US-0899660.  
PR 01-JUL-1992; 92US-0907224.  
PR 27-OCT-1992; 92US-0966775.  
XX  
PA (IMMV ) IMMUNEX CORP.  
XX  
PI Armitage RJ, Goodwin RG, Smith CA;

```

XX
DR WPI; 1993-405417/50.
DR N-PSDB; AAQ53536.
XX
XX New cytokine, CD30-L, which binds CD30 - used for developing
XX prods. for diagnosis, detection, purifications, research and
XX therapy
XX
XX Claim 15; Figure 5a; 59pp; English.
PS
PS CD30-L is a ligand for CD30, the 120kd surface antigen widely used
CC as a clinical marker for Hodgkin's lymphoma and related haematologic
CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
CC L and other derived prods. can be used for elucidating the roles
CC that CD30 and CD30-L may play in the immune system and for diagnosis
CC and therapy. It can be isolated as follows. A cDNA library prep.d. from
CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L.
CC This cDNA can then be used as a probe to screen a human PBL cDNA
CC library to obtain cDNA encoding human CD30-L.
XX
XX Sequence 215 AA;
XX
Query Match 100.0%; Score 1118; DB 14; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.7e-116;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHVPAGSVASHLGTTSRSYFYLTTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLPG 60
Db 1 mhvpagsvashlgttsrsyfyllttatlalclvftvatimvlvqrtdsipnsdpnvpkg 60
XX
QY 61 GNCSEDLILCKRAPFKKSWAYLQVAKHLNKTLSWNKDGILHGVRYQDGNLVIQFPGLY 120
Db 61 gncsedlilckrapfkkswaylqvakhlnktlswnkdgilhgvryqdglnviqfpgly 120
XX
QY 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKQALVTVCESGMOTKHVYQNLSQFLLDYLQ 180
Db 121 fiicqlqlvqcpnnsvdllkllinkhikqalvtvcsgmqtkhvyqnlsgflldylq 180
XX
QY 181 VNTTISVNVDTFQYIDTSTFPLENVLISFLYSNSD 215
Db 181 vnttisvnavdtfqyidstfplenvlslflysnsd 215
XX
RESULT 2
AAR45009
ID AAR45009 standard; Protein; 234 AA.
XX
XX AAR45009;
XX
XX 19-JUN-1994 (first entry)
XX
XX Sequence encoded by a human CD30-L cDNA clone
DE encoding additional N-terminal amino acids.
XX
XX Hodgkin's disease; lymphoma; surface antigen; cytokine;
KW CD30 ligand; CD30-L; TNF; NGF.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH 41..62
FT /label= Transmembrane
XX
XX WO9324135-A.
XX
XX 09-DEC-1993.
XX
XX 25-MAY-1993; 93WO-US04926.
XX
XX 26-MAY-1992; 92US-0889717.
PR 02-JUN-1992; 92US-0892459.

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PR 15-JUN-1992; 92US-0899560.
PR 01-JUL-1992; 92US-0907224.
PR 27-OCT-1992; 92US-0966775.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Armitage RJ, Goodwin RG, Smith CA;
PI
XX WPI; 1993-405417/50.
DR N-PSDB; AAQ53538.
XX
XX New cytokine, CD30-L, which binds CD30 - used for developing
XX prods. for diagnosis, detection, purifications, research and
XX therapy
XX
XX Claim 15; Figure 7a; 59pp; English.
PS
PS CD30-L is a ligand for CD30, the 120kd surface antigen widely used
CC as a clinical marker for Hodgkin's lymphoma and related haematologic
CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
CC L and other derived prods. can be used for elucidating the roles
CC that CD30 and CD30-L may play in the immune system and for diagnosis
CC and therapy. It can be isolated as follows. A cDNA library prep.d. from
CC the murine helper T-cell line 7B9 is screened with a CD30/Fc fusion
CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L
CC (AAQ53535). This cDNA can then be used as a probe to screen a human PBL
CC cDNA library to obtain cDNA encoding human CD30-L (AAQ53536). An
CC anchored PCR technique was employed to isolate CD30-L human and murine
CC clones containing an additional 19 N-terminal amino acid sequence
CC (AAQ53537, AAQ53538).
XX
XX Sequence 234 AA;
XX
Query Match 100.0%; Score 1118; DB 14; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.9e-116;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHVPAGSVASHLGTTSRSYFYLTTATLALCLVFTVATIMVLVQRTDSIPNSPDNVLPG 60
Db 20 mhvpagsvashlgttsrsyfyllttatlalclvftvatimvlvqrtdsipnsdpnvpkg 79
XX
QY 61 GNCSEDLILCKRAPFKKSWAYLQVAKHLNKTLSWNKDGILHGVRYQDGNLVIQFPGLY 120
Db 80 gncsedlilckrapfkkswaylqvakhlnktlswnkdgilhgvryqdglnviqfpgly 139
XX
QY 121 FIICQLQFLVQCPNNSVDLKLLELLINKHKQALVTVCESGMOTKHVYQNLSQFLLDYLQ 180
Db 140 fiicqlqlvqcpnnsvdllkllinkhikqalvtvcsgmqtkhvyqnlsgflldylq 199
XX
QY 181 VNTTISVNVDTFQYIDTSTFPLENVLISFLYSNSD 215
Db 200 vnttisvnavdtfqyidstfplenvlslflysnsd 234
XX
RESULT 3
AAR45006
ID AAR45006 standard; Protein; 220 AA.
XX
XX AAR45006;
XX
XX 19-JUN-1994 (first entry)
XX
XX Sequence encoded by a murine CD30-L cDNA clone.
DE
XX Hodgkin's disease; lymphoma; surface antigen; cytokine;
KW CD30 ligand; CD30-L; TNF; NGF.
XX
XX Acomys cahirinus.
XX
XX Key Location/Qualifiers
FH 28..48
FT /label= transmembrane

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XX WO9324135-A.
XX PD 09-DEC-1993.
XX PF 25-MAY-1993; 93WO-US04926.
XX PR 26-MAY-1992; 92US-0889717.
XX PR 02-JUN-1992; 92US-0892459.
XX PR 15-JUN-1992; 92US-0899660.
XX PR 01-JUL-1992; 92US-0907224.
XX PR 27-OCT-1992; 92US-0966775.
XX PA (IMMV ) IMMUNEX CORP.
XX PI Armitage RJ, Goodwin RG, Smith CA;
XX WPI; 1993-405417/50.
XX DR N-PSDB; AAQ53535.
XX PT New cytokine, CD30-L, which binds CD30 - used for developing
XX PT prods. for diagnosis, detection, purifications, research and
XX PT therapy
XX PS Claim 15; Figure 3a; 59pp; English.
XX CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
XX CC as a clinical marker for Hodgkin's lymphoma and related haematologic
XX CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
XX CC L and other derived prods. can be used for elucidating the roles
XX CC that CD30 and CD30-L may play in the immune system and for diagnosis
XX CC and therapy. It can be isolated as follows. A cDNA library prep.d. from
XX CC the murine helper T-cell line 7B9 is screened with a CD30/FC fusion
XX CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L.
XX CC This cDNA can then be used as a probe to screen a human PBL cDNA
XX CC library to obtain cDNA encoding human CD30-L.
XX SQ Sequence 220 AA;
Query Match 72.9%; Score 814.5; DB 14; Length 220;
Best Local Similarity 70.6%; Pred. No. 1.2e-82;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;
QY 1 MHVPAGSVAS-----HLGTTSRSYFYLTATLALCLVFTVATIMVLVQRTDSIPNSPD 54
Db 1 mqvpgsvasprwstrprwstrsrsfyfisttal-vclvvavailvlvqkdstpntte 59
QY 55 NVPLKGGNCSEDLCLILKRAPKKSWAYLQVAKHLNKTLSWNKDGILHGVRYQDGNLVI 114
Db 60 kaplkgncsedlftlktstpskkswaylqvskhlnntklswnedgtihglyqdnliv 119
QY 115 QPGLYFIICQLQFLVQCPCNNSVDLKLLELLINKHKIKQALVTVCESGMQTKHYQNLISQF 174
Db 120 qfpglyfivcqlqflvqcshnsdvdlclqllnskikkqtlvtvcesgvqskniyqnsqf 179
QY 175 LLDYLQVNTTISVNVDTFYIDTSTFPLENVLISFLYSNSD 215
Db 180 llhylvqnvstisvrndfnfyvdtntfpldnvlsvflysssd 220
RESULT 4
AAR45008
ID AAR45008 standard; Protein; 239 AA.
XX AC AAR45008;
XX DT 19-JUN-1994 (first entry)
XX DE Sequence encoded by a murine CD30-L cDNA clone
XX DE encoding additional N-terminal amino acids.
XX KW Hodgkin's disease; lymphoma; surface antigen; cytokine;

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```

KW CD30 ligand; CD30-L; TNF; NGF.
XX Acomys cahirinus.
XX FH Key Location/Qualifiers
XX FT 47..67
XX FT /label= Transmembrane
XX PN WO9324135-A.
XX PD 09-DEC-1993.
XX PF 25-MAY-1993; 93WO-US04926.
XX PR 26-MAY-1992; 92US-0889717.
XX PR 02-JUN-1992; 92US-0892459.
XX PR 15-JUN-1992; 92US-0899660.
XX PR 01-JUL-1992; 92US-0907224.
XX PR 27-OCT-1992; 92US-0966775.
XX PA (IMMV ) IMMUNEX CORP.
XX PI Armitage RJ, Goodwin RG, Smith CA;
XX WPI; 1993-405417/50.
XX DR N-PSDB; AAQ53537.
XX PT New cytokine, CD30-L, which binds CD30 - used for developing
XX PT prods. for diagnosis, detection, purifications, research and
XX PT therapy
XX PS Claim 15; Figure 6a; 59pp; English.
XX CC CD30-L is a ligand for CD30, the 120kd surface antigen widely used
XX CC as a clinical marker for Hodgkin's lymphoma and related haematologic
XX CC malignancies. CD30 is a member of the TNF/NGF superfamily. The CD30-
XX CC L and other derived prods. can be used for elucidating the roles
XX CC that CD30 and CD30-L may play in the immune system and for diagnosis
XX CC and therapy. It can be isolated as follows. A cDNA library prep.d. from
XX CC the murine helper T-cell line 7B9 is screened with a CD30/FC fusion
XX CC protein labelled with (125)I to obtain cDNA encoding murine CD30-L
XX CC (AAQ53535). This cDNA can then be used as a probe to screen a human PBL
XX CC cDNA library to obtain cDNA encoding human CD30-L (AAQ53536). An
XX CC anchored PCR technique was employed to isolate CD30-L human and murine
XX CC clones containing an additional 19 N-terminal amino acid sequence
XX CC (AAQ53537, AAQ53538).
XX SQ Sequence 239 AA;
Query Match 72.9%; Score 814.5; DB 14; Length 239;
Best Local Similarity 70.6%; Pred. No. 1.3e-82;
Matches 156; Conservative 26; Mismatches 32; Indels 7; Gaps 2;
QY 1 MHVPAGSVAS-----HLGTTSRSYFYLTATLALCLVFTVATIMVLVQRTDSIPNSPD 54
Db 20 mqvpgsvasprwstrprwstrsrsfyfisttal-vclvvavailvlvqkdstpntte 78
QY 55 NVPLKGGNCSEDLCLILKRAPKKSWAYLQVAKHLNKTLSWNKDGILHGVRYQDGNLVI 114
Db 79 kaplkgncsedlftlktstpskkswaylqvskhlnntklswnedgtihglyqdnliv 138
QY 115 QPGLYFIICQLQFLVQCPCNNSVDLKLLELLINKHKIKQALVTVCESGMQTKHYQNLISQF 174
Db 139 qfpglyfivcqlqflvqcshnsdvdlclqllnskikkqtlvtvcesgvqskniyqnsqf 198
QY 175 LLDYLQVNTTISVNVDTFYIDTSTFPLENVLISFLYSNSD 215
Db 199 llhylvqnvstisvrndfnfyvdtntfpldnvlsvflysssd 239
RESULT 5
AAB08276

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[illegible]



DE Mouse Fas ligand (partial sequence).  
 XX  
 KW Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;  
 KW Fas cell surface antigen; Fas-L; mouse.  
 XX  
 OS Mus musculus.  
 XX  
 XX  
 PN WO9513293-A1.  
 XX  
 XX 18-MAY-1995.  
 XX  
 PF 10-NOV-1994; 94WO-JP01899.  
 XX  
 XX 18-OCT-1994; 94JP-0278378.  
 PR 10-NOV-1993; 93JP-0305975.  
 PR 13-DEC-1993; 93JP-0342526.  
 PR 18-MAR-1994; 94JP-0074344.  
 PR 08-JUL-1994; 94JP-0180955.  
 PR 07-SEP-1994; 94JP-0239363.  
 XX  
 XX (MOCH ) MOCHIDA PHARM CO LTD.  
 PA (OSAB-) OSAKA BIOSCIENCE INST.  
 XX  
 PI Nagata S, Nakamura N, Suda T, Takahashi T;  
 XX  
 DR WPI; 1995-194031/25.  
 DR N-PSDB; AAQ99497.  
 XX  
 XX Peptide which binds to Fas antigen, and antibody reactive with it -  
 PT for treatment and diagnosis of viral or auto:immune diseases  
 PT  
 XX  
 PS Claim 10; Page 221-222; 300pp; Japanese.  
 XX  
 XX Fas ligands or active fragments able to induce apoptosis in cells  
 CC which express the Fas cell surface antigen are claimed. The  
 CC proteins are isolated from human, rat and mouse sources. The present  
 CC sequence represents part of the mouse Fas ligand.  
 XX  
 SQ Sequence 138 AA;  
 Query Match 9.5%; Score 106; DB 16; Length 138;  
 Best Local Similarity 25.2%; Pred. NO. 0.00056;  
 Matches 31; Conservative 22; Mismatches 46; Indels 24; Gaps 4;  
 QY 78 KSWAYLOVAKHLNKTLSWKNK---DGLHGVRVODGNLVIOFPGLYFIICQLQFLVO-CP 133  
 Db 1 rsvahltgnphsrsipledtygtalisgvykkgglvlnetglyfyvskvyfrgscn 60  
 QY 134 NNSVDLKLELLINKH-----IKKQALVTVCESGM-----QTKHVTYONLSQ 173  
 Db 61 ngplnhkvymrnskyppedivlmeekrlnycttggiwahssylgavfnltsadhllyvnisq 120  
 QY 174 FLL 176  
 Db 121 ls1 123  
 RESULT 12  
 AAR79067  
 ID AAR79067 standard; Protein; 137 AA.  
 XX  
 AC AAR79067;  
 XX  
 DT 22-FEB-1996 (first entry)  
 XX  
 DE Mouse Fas ligand (partial sequence).  
 XX  
 KW Fas ligand; Tumour Necrosis factor family; apoptosis; cell death;  
 KW Fas cell surface antigen; Fas-L; mouse.  
 XX  
 OS Mus musculus.  
 XX

PN WO9513293-A1.  
 XX  
 PD 18-MAY-1995.  
 XX  
 PF 10-NOV-1994; 94WO-JP01899.  
 XX  
 XX 18-OCT-1994; 94JP-0278378.  
 PR 10-NOV-1993; 93JP-0305975.  
 PR 13-DEC-1993; 93JP-0342526.  
 PR 18-MAR-1994; 94JP-0074344.  
 PR 08-JUL-1994; 94JP-0180955.  
 PR 07-SEP-1994; 94JP-0239363.  
 XX  
 XX (MOCH ) MOCHIDA PHARM CO LTD.  
 PA (OSAB-) OSAKA BIOSCIENCE INST.  
 XX  
 PI Nagata S, Nakamura N, Suda T, Takahashi T;  
 XX  
 DR WPI; 1995-194031/25.  
 DR N-PSDB; AAQ99496.  
 XX  
 XX Peptide which binds to Fas antigen, and antibody reactive with it -  
 PT for treatment and diagnosis of viral or auto:immune diseases  
 PT  
 XX  
 PS Claim 9; Page 219-221; 300pp; Japanese.  
 XX  
 XX Fas ligands or active fragments able to induce apoptosis in cells  
 CC which express the Fas cell surface antigen are claimed. The  
 CC proteins are isolated from human, rat and mouse sources. The present  
 CC sequence represents part of the mouse Fas ligand.  
 XX  
 SQ Sequence 137 AA;  
 Query Match 9.3%; Score 104; DB 16; Length 137;  
 Best Local Similarity 25.4%; Pred. NO. 0.00093;  
 Matches 31; Conservative 21; Mismatches 46; Indels 24; Gaps 4;  
 QY 79 SWAYLOVAKHLNKTLSWKNK---DGLHGVRVODGNLVIOFPGLYFIICQLQFLVO-CPN 134  
 Db 1 svahltgnphsrsipledtygtalisgvykkgglvlnetglyfyvskvyfrgscn 60  
 QY 135 NSVDLKLELLINKH-----IKKQALVTVCESGM-----QTKHVTYONLSQF 174  
 Db 61 qplnhkvymrnskyppedivlmeekrlnycttggiwahssylgavfnltsadhllyvnisq 120  
 QY 175 LL 176  
 Db 121 sl 122  
 RESULT 13  
 AAR77282  
 ID AAR77282 standard; Protein; 279 AA.  
 XX  
 AC AAR77282;  
 XX  
 DT 05-DEC-1995 (first entry)  
 XX  
 DE Mouse Fas-L protein.  
 XX  
 KW Fas ligand; Fas-L; cell surface protein; autoimmune disease;  
 KW self-tolerance.  
 XX  
 OS Mus sp.  
 XX  
 PH Key Location/Qualifiers  
 FT Domain 1..78  
 FT /label= Cytoplasmic\_domain  
 FT 79..103  
 FT /label= Transmembrane\_domain  
 FT 104..279  
 FT /label= Extracellular\_domain

P	N		W09821232-A2.	
X	X			
P	D		22-MAY-1998.	
X	F			
P	F		13-NOV-1997; 97WO-US20864.	
X	X			
P	R		12-NOV-1997; 97US-0968686.	
X	X		13-NOV-1996; 96US-0030871.	
P	R		10-FEB-1997; 97US-0039972.	
X	X			
P	A		(CHIR ) CHIRON CORP.	
X	X			
P	I		Chu K;	
X	X			
D	R		WPI; 1998-297861/26.	
D	R		N-PSDB; AAV32622.	
X	X			
P	T		New DNA encoding Fas ligand agonist including, e.g. deletion -	
P	T		useful for, e.g. treating auto-immune diseases or transplant	
P	T		rejection	
X	X			
P	S		Claim 4; Pages 62-63; 72pp; English.	
X	X			
C	C		The present sequence represents a non-cleavable Fas ligand 1306142	
C	C		deltion mutein. Fas ligand deletion mutein can be expressed in	
C	C		cells transfected with the DNA (AAV32622) coding for the mutant protein.	
C	C		These cells, expressing the mutant Fas ligand in a non-cleavable form,	
C	C		are claimed to be useful in vitro to identify cells that express Fas	
C	C		and, in vivo or in vitro, for reducing proliferation of Fas-expressing	
C	C		cells. The DNA encoding the Fas ligand mutant is claimed to be	
C	C		useful in gene therapy procedures and for the treatment of autoimmune	
C	C		diseases, e.g. multiple sclerosis, erythematosus, rheumatoid arthritis,	
C	C		glomerulonephritis, myasthenia gravis and transplant rejection.	
X	X			
S	O		Sequence 268 AA;	
			Query Match 8.7%; Score 97; DB 19; Length 268;	
			Best Local Similarity 22.4%; Pred. No. 0.015;	
			Matches 45; Conservative 27; Mismatches 55; Indels 74; Gaps 9;	
Qy	49	IPNSFDNVPL-----KGCNGSEDLCLTL-----KRA 74		
	:	:		
Db	54	lppppppplpplpplpkkrghstg-lcillvmfmlvalvglgimqflhlqkela 112		
	:	:		
Qy	75	PFKSWAYLOWAKHLNKT-----LSNKD-GI--LHGVRVODGNLVIOF 116		
	:	:  :   :   :   :   :		
Db	113	elrestqgmhtasslekirkvahltgksnrsmplewedyglvlsgvkykkgglvine 172		
	:	:  :   :   :   :   :		
Qy	117	PGLYFIICQLFLVQ-CPNNSVDLKLELLINKH-----IKQALVTVCESGM----- 162		
	:	:  :   :   :   :   :   :   :   :		
Db	173	tglyfvyskyfyrgscnnlpishkvymrnskyqqdlmmegkmmscycttgqmwarssyl 232		
	:	:  :   :   :   :   :		
Qy	163	-----OTRHVYQNLSOFL 176		
	:	:  :   :   :   :   :		
Db	233	gavnlttsadhlyvnvselsl 253		
	:	:  :   :   :   :   :		
RESULT 15				
AAW48954				
ID	AAW48954 standard; Protein; 265 AA.			
X	X			
AC	AAW48954;			
X	X			
D	T		23-SEP-1998 (first entry)	
X	X			
DE	DE		Non-cleavable Fas ligand 1306145 deletion mutein.	
X	X			
KW	KW		Non-cleavable Fas ligand 1306145 deletion mutein; Fas; erythematosus;	
KW	KW		gene therapy; autoimmune disease; multiple sclerosis;	
KW	KW		rheumatoid arthritis; myasthenia gravis; transplant rejection;	
X	X		glomerulonephritis.	

```
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Region 1..129
FT FT /note= "represents residues 1-129 of the wild-type
FT FT Fas ligand"
FT Region 130..265
FT FT /note= "represents residues 146-281 of the
FT FT wild-type Fas ligand"
XX
PN WO9821232-A2.
XX
PD 22-MAY-1998.
XX
PP 13-NOV-1997; 97WO-US20864.
XX
PR 12-NOV-1997; 97US-0968686.
PR 13-NOV-1996; 96US-0030871.
PR 10-FEB-1997; 97US-0039972.
XX
PA (CHIR ) CHIRON CORP.
XX
PI Chu K;
XX
DR WPI; 1998-297861/26.
DR N-PSDB; AAV32623.
XX
PT New DNA encoding Fas ligand agonist including, e.g. deletion -
PT useful for, e.g. treating auto-immune diseases or transplant
PT rejection
XX
PS Claim 4; Pages 65-66; 72pp; English.
XX
CC The present sequence represents a non-cleavable Fas ligand 1306145
CC deletion mutein. Fas ligand deletion mutein can be expressed in
CC cells transfected with the DNA (AAV32623) coding for the mutant protein.
CC These cells, expressing the mutant Fas ligand in a non-cleavable form,
CC are claimed to be useful in vitro to identify cells that express Fas
CC and, in vivo or in vitro, for reducing proliferation of Fas-expressing
CC cells. The DNA encoding the Fas ligand mutant is claimed to be
CC useful in gene therapy procedures and for the treatment of autoimmune
CC diseases, e.g. multiple sclerosis, erythematosis, rheumatoid arthritis,
CC glomerulonephritis, myasthenia gravis and transplant rejection.
XX
SQ Sequence 265 AA;

Query Match 8.6%; Score 96.5; DB 19; Length 265;
Best Local Similarity 22.7%; Pred. No. 0.016;
Matches 45; Conservative 26; Mismatches 56; Indels 71; Gaps 9;

QY 49 IPNSPDNVPL-----KGNCSDDLICIL-----KRA 74
   :| | | | | | | | | | | | | | | | | | | | |
Db 54 lpppppppplpplpplpplkrgnhstg-lcllvmffmvlvalvglgmfglfhlqkela 112
   :| | | | | | | | | | | | | | | | | | | | |
QY 75 PPKKSWAYLQVAKHLNKT-----KLSWNKD-GI--LHGVRVQDGNLVIOFPGL 119
   :| | | | | | | | | | | | | | | | | | | | |
Db 113 elrestsqmhtasslekvahlgtgksnrsmplewedtygivilsgvkykkgglvinetgl 172
   :| | | | | | | | | | | | | | | | | | | | |
QY 120 YFTICOLQFLVQ-CPNNSVDLKLLELINKH-----TKQALVTVCESGM----- 162
   :| | | | | | | | | | | | | | | | | | | | |
Db 173 yfvyskvyfrgscnnlpishkvymrnskyppqdlvmmegkmsyscttgqmwarssylgav 232
   :| | | | | | | | | | | | | | | | | | | | |
QY 163 ----QTKHVVQNLSQFL 176
   :| | | | | | | | | | | | | | | | | | | | |
Db 233 fnltsadhlyvnnvselsl 250
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